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Access DB# \_\_\_\_\_

#### SEARCH REQUEST FORM

#### Scientific and Technical Information Center

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Requester's Full Name: Station Art Unit: Phone I Mail Pay and Pldg/Page I continue	Number 20 8 September 20	Examiner #: 275 3	Pate:
Mail Box and Bldg/Room Location	n: 8/3/8/29 Res	sults Format Preferred (circle): P	APER DISK E-MAIL
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If more than one search is subm	nitted, please prioriti		i. *******
Please provide a detailed statement of the Include the elected species of structures, I utility of the invention. Define any terms known. Please attach a copy of the cover	keywords, synonyms, acro that may have a special m sheet, pertinent claims, an	e as specifically as possible the subject myms, and registry numbers, and com neaning. Give examples or relevant ci d abstract.	t matter to be searched. bine with the concept or
Title of Invention:	My fact 6		
Inventors (please provide full names):	Patrela	<u> </u>	<u> </u>
	,		CCV.
Earliest Priority Filing Date:	12/11/97		
*For Sequence Searches Only* Please inclu	de all pertinent information	(parent, child, divisional, or issued paten	t numbers) along with the
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OM protein – protein search, using sw model

January 24, 2003, 12:21:10 ; Search time 37 Seconds (without alignments) 1364.919 Million cell updates/sec Run on:

US-09-944-457-2 1992 Perfect score:

1 MKEYVLLLFLALCSAKPFFS.

Sequence:

......PATFRCVLSRMSVQLGNFGM 379

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

908470 Total number of hits satisfying chosen parameters:

908470 seqs, 133250620 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries

Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		Human PRO241 polyp	Human PRO241 polyp	Human andiodenesis	Human PRO241 prote	Human PRO241 prote	Mouse bone/cartila	Murine protein iso	Human polypeptide	Novel human diagno	Human protein sequ
SUMMARIES			ID			AAU12335	ABB95437	ABB84831	AAY17820	AAE05347	ABB72356	AAM40351	ABG22569	AAB95678
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### ALIGNMENTS

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PRO; membrane bound protein; secreted protein; PRO357; PRO327; PRO243; PRO454; PRO343; PRO545; PRO545; PRO545; PRO555; PRO555; PRO555; PRO555; PRO555; PRO555; PRO556; PRO556; PRO565; PRO565; PRO565; PRO566; PRO566; PROFE
                                                                                                                                                                                                                                                        /label = Leucine zipper pattern
210..216
/note= " N-myristoylation site"
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/note= "N-myristoylation site"
154..176
                                                                                                                                                                                                          /label= Signal peptide
                                                                                                                                                                                       Location/Qualifiers
                      AAB01311 standard; Protein; 379 AA.
                                                                  (first entry)
                                                                                      Human PRO241 polypeptide.
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                                                                25-SEP-2000
                                                                                                                                                                    Homo sapiens
                                            AAB01311;
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RESULT 1
           AAB01311
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/note= "N-myristoylation site"

301 KKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQP 360

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptides which are designated as PRO polypeptides are described The membrane-bound proteins have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. Anti-PRO antibodies are useful for the affinity purification of PRO from recombinant cell culture or natural sources.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human nucleic acids encoding secreted and transmembrane polypeptides, designated as PRO polypeptides, useful as pharmaceutical
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Napier MA, Roy MA, Tumas D, Wood WI;
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               'note= "N-myristoylation site"
                                           "N-myristoylation site"
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281..285
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/note= "N-glycosylation site"
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ME, Goddard A,
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Best Local Similarity 100./
Matches 379; Conservative
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Gerritsen ME,
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Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deforge L, Desnoyers L, Filvaroff E, C
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                               AAU12335 standard; Protein; 379 AA.
                                                                                                                                                  Human PRO241 polypeptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lung, breast, prostate, cervical
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99WO-US30999.
99WO-US31243.
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2000WO-US08439.
2000WO-US13705.
2000WO-US14042.
2000WO-US14941.
361 ATFRCVLSRMSVQLGNFGM 379
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99US-0170262.
99WO-US30095.
                     361 ATFRCVLSRMSVOLGNFGM 379
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20-DEC-1999;
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30-MAR-2000;
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                                                      RESULT 2
AAU12335
QY
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Claim 12; Fig 328; 813pp; English.

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PRO polypeptides. The PRO polypeptides are useful to detect other. PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TMF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation of chondrocytes, the proliferation of artilage, the proliferation of a cytokine from peripheral blood of T-lymphocytes, the release of a cytokine from peripheral blood the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     379 AA;
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Homo sapiens

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One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal
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Stephan JF, Watanabe CK, Williams PM, Wood WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerber H, Gerritsen ME,
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2001US-0816744.
2001US-0828366.
2001US-0854208.
2001US-0854280.
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2000US-070923B.
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2001US-0767609.
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2001WO-US06520.
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2001US-0802706.
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2001US-0866034,
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2001WO-US17443.
                                          09-JUL-2001; 2001WO-US21735
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GODOWSKI P J.
GURNEY A L.
HILLAN K J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baker KP, Ferrara N,
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                                                                                                                                                                                                                                                                                                                                                                                                GENENTECH INC
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STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-171999/22.
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FERRARA N.
                                                                                                                                                                                                                                                                                                                                                                                                                         GERBER H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WOOD W I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABL95575.
       WO200208284-A2
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25-MAY-2001;
25-MAY-2001;
30-MAY-2001;
30-MAY-2001;
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                                                                                                             23-AUG-2000;
24-AUG-2000;
07-SEP-2000;
                                                                                                                                       15-SEP-2000;
18-SEP-2000;
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17-AUG-2000;
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09-MAR-2001;
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24-OCT-2000;
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10-MAY-2001;
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                        31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GURN/) (HILL/) (MARS/)
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(WOOD/) V
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                                                                                   hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tunmour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a PRO protein of the invention.
                                   The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; anylogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthrists; myocardial infarction; thrombophlebitis; lymphangitis; tumour anglogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
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                                                                                                                                                                                                                                                                                                                                                                                            61 PRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEND 120
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                                                                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                                    0; Mismatches
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Claim 11; Fig 30; 567pp; English.
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                                                                                                                                                                                                                                                                    Matches 379; Conservative
                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                               379 AA;
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ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL08259 to ABL88267 represent primers and probes used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF; Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal
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                                                                                                                                                                                                                                                                                                  001WO-US06520.
                                                      2000WO-US20710.
                                                                                                                                                         000US-0665350.
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000WO-US32678.
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2001WO-US17443.
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2001US-0866034
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28-FEB-2001;
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02-AUG-2000;
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18-SEP-2000;
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10-NOV-2000;
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Stephan JF,
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0; Gaps

0; Indels

100.0%; Score 1992; DB 2: 100.0%; Pred. No. 4e-177; tive 0; Mismatches 0

Conservative

Matches 379;

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Query Match Best Local

Similarity

DB 23; Length 379;

1 MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDFFPTRE 60

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KVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPP 240
                                    PRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEND 120
                                                              FKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHEN 180
                                                                                                                                     TLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKL 300
                                                                                                                                                                         KKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQP 360
Human; PRO protein; tumour necrosis factor family; INF; cytokine; secreted protein; transmembrane protein; inflammation disorder.
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                                                                                                                                                                                                                                                                         AAY17820 standard; Protein; 379 AA.
                                                                                                                                                                                                                                                                                                                               Human PRO241 protein sequence
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9705-0069278.
9705-0069334.
9705-0069425.
9705-0069694.
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97US-0069870.
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N-PSDB; AAX80043.
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16-DEC-1997;
16-DEC-1997;
16-DEC-1997;
17-DEC-1997;
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09-FEB-1998,
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                                                                            transmembrane proteins used therapeutically. The PRO proteins have eyrostatic, anti-inflammatory, anti-proliferative and immunosuppressive activity. The proteins and polynucleotides can be used in therapy, identification of homologues, raising antibodies and design of probes and primars. They can be used in a range of diseases related to proteins that they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses.
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                                                             The present invention describes nucleic acids encoding PRO secreted and
                                                                                                                                                                                                                                                                                                                                                                              PRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEND 120
                                                                                                                                                                                                                                                                                                                                                                                                                          121 FKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHEN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TILLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQP 360
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                 MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDTFPTRE
                                                                                                                                                                                                                                                                                                                               1 MKEYVLLIFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDTRFPTRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 KVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPP
                                                                                                                                                                                                                                                                    .;
0
Nucleic acids encoding PRO secreted and transmembrane proteins
                                                                                                                                                                                                                                   Length 379;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse bone/cartilage proteoglycan I (BGN) protein.
                                                                                                                                                                                                                                   99.9%; Score 1990; DB 20;
99.7%; Pred. No. 6.2e-177;
Live 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE05347 standard; Protein; 373 AA.
                              Claim 12; Fig 2; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATFRCVLSRMSVQLGNFGM 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 ATFRCVLSRMSVQLGNFGM 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-DEC-2000; 2000WO-NZ00256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-1999; 99US-0171678.
28-NOV-2000; 2000US-0724864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.77
Matches 378; Conservative
                                                                                                                                                                                                      379 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE05347;
                                                                                                                                                                                                        Sequence
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   qq
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355 ATFRCVLGRMSVQLGNVG 372

qq

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Watson JD, Murison JG;

XW Watson JD, Murison JG;

XW WEI; 2001-42566545.

BN P-SDB; AAD10114.

XX WEI; 2001-42566545.

RN P-SDB; AAD10114.

XX Novel isolated polypeptide useful to isolate corresponding interacting proteins or other compounds, to quantitatively determine levels of interacting proteins or other compounds, and as therapeutic target.

PT proteins or other compounds, and as therapeutic target.

XX Claim 6; Page 76-77; 101pp; English.

XX The patent discloses novel polynucleotides and their corresponding proteins which play a major role in induction of growth, cell migration cell claim and proliferation, cell-cell interaction and the differentiation of tissue-specific cells. These proteins are important in the maintenance of tissue integrity and thus are important in the maintenance consecution sasays to determine the biological activity, to raise multibodies, to isolate corresponding interacting proteins or there compounds, and as therapeutic target in a whole angling of disease corresponding interacting proteins or other compounds, to quantitatively determine levels of interacting proteins or other compounds, and as therapeutic target in a whole range of disease corresponding interacting proteins or other compounds, to age and physical mapping, in positional cloning of disease to tag or identify an organism or its reproductive material (as non-disruptive tags for marking organism or its reproductive material (as non-disruptive tags for marking organisms), and for the diagnosis and correspondent of a vaccine or anti-cancer treatment, as target for cancer treatment, as immunorequiatory and anti-inflammatory molecule, as a part of a vaccine or anti-cancer treatment, as target for cancer treatment, and as a target for anometure of diseases such as a starget for anometure of diseases such as a starget for anometure of diseases such as a starget for anometure the activity of the soluble molecule that binds protein from mouse. BGN is also known as bidlycan or PG-SI.

The present sequence is bone/cartilag
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SQ Sequence 373 AA;
Query Match 90.3%; Score 1799; DB 22; Length 373;
Best Local Similarity 90.2%; Pred. No. 3.9e-159;
Matches 341; Conservative 17; Mismatches 14; Indels 6; Gaps

ij

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Gaps

Indels

14;

17; Mismatches

341; Conservative

Matches

Db Qy Db

Query Match Best Local Similarity 181 KVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPP 240

q

ò

q

361 ATFRCVLSRMSVQLGNFG 378

90.3%; Score 1799; DB 23; Length 373; 90.2%; Pred. No. 3.9e-159;

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isolated from human, murine and rat skin cell libraries. The sequences can be used in the development of therapeutic agents useful in the treatment of skin diseases, including skin wounds, cancer, growth defects, developmental defects and inflammatory diseases. The proteins have important roles in the induction of hair growth, cell proliferation healing and cell-cell interaction, in maintaining tissue integrity, in wound healing and in modulating immune responses. The present sequence is a polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides the protein and coding sequences of cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sleeman M, Onrust R, Murison JG, Kumble KD;
                                                                                                                                                                                      Human; rat; mouse; skin cell; skin wound; cancer; growth defect; developmental defect; inflammatory disease; dermatological; vulnerary; immunomodulator; anti-inflammatory; cytostatic; neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides and polypeptides encoded by the polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isolated from skin cells, useful for treating skin wounds, cancers, growth and developmental defects, inflammatory diseases, or for
                                                                                                                                                    Murine protein isolated from skin cells SEQ ID NO: 680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 434-435; 466pp; English.
                                    ABB72356 standard; Protein; 373 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JUL-2000; 2000US-221232P.
                                                                                                                                                                                                                                                                                                                                                                                     24-MAY-2001; 2001WO-NZ00099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modulating immune responses
                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAY-2000; 2000US-206650P
                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Watson JD, Strachan L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-122020/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               373 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABL35045.
                                                                                                                                                                                                                                                                                                             WO200190357-A1.
                                                                                                              04-APR-2002
                                                                                                                                                                                                                                                                                                                                               29-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sednence
                                                                          ABB72356;
RESULT 7
                  ABB72356
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Drmanac RT, Liu C,
                                                                                                   Local Similarity
les 316; Conserv
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                                                                   344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200175067-A2.
                                           specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biodiversity
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                                                                    Sequence
                                                                                          Query Match
                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                          296
                                                                                                                                                                                                                                                                                                                                                                                             321
                                  Note:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
                                                                                                                                                                                                                                                                           Human, nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosls; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   á
                                                        KKIPSGLPELKYLOIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQP 360
          241 TLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKL 300
                                                                     Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries \boldsymbol{\cdot}
                         Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen R, Ma Y, Xu C, Xue AJ, R, Drmanac RT;
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                                                                                                                                                                                   AAM40351 standard; Protein; 344 AA
                                                                                                                                                                                                                                                      Human polypeptide SEQ ID NO 3496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C, Asundi V, Ch
Wang Z, Wehrman T, X:
Zhou P, Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0662191.
19-OCT-2000; 2000US-0693036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-0620312.
                                                                                                                                                                                                                                                                                                                                                                                                                               26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0727344
                                                                                                     ATFRCVLSRMSVQLGNFG 378
                                                                                                                 22-OCT-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAI59507
                                                                                                                                                                                                                                                                                                                                                                                  WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                         26-JUL-2001
                                                                                                                                                                                                                                                                                                                                       leukaemia.
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                                                                                                                                                                                                         AAM40351;
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                                                                                                                                                             RESULT 8
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ID AAM
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and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                 The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 IKENDFKGLTSLYGLILNNNKLTKIHPRAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAEL 140
                                                                                                                                                                                                                                                                                                                                  56 FPTREPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                          116 IKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAEL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVP 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKY 355
                                                                                                                                                                                                                                                                                                                                                                                   21 FQQESQEAIFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKE 80
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                   Length 344;
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                   Score 1649; DB 22;
Pred. No. 3.3e-145;
1; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   356 WEMOPATFRCVLSRMSVQLGNFGM 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG22569 standard; Protein; 352
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                                                                                                                                                                                                                      82.8%;
ilarity 97.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2001; 2001WO-US08631.
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23-AUG-2000; 2000US-0649167.
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N-PSDB; AAS86756.
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polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as
                                                                                                                                                                                                           a food supplement. [11] and its binding partners are useful in medical imaging of sites expressing [II]. [I) and [II] are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 FPTREPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233
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                                                                                                                                                                                                                                                                                                                                  and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 FQGESQEAIFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIHENKVKKIQKDTFKGMNALHVLEMSANPLDNN-GIEPGAF-EGVTVFHIRIAEAKLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGIGNNKITDIENGSLANIPRVREI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.2%; Score 1558; DB 22; Length 352; 93.6%; Pred. No. 1.1e-136; Live 3; Mismatches 16; Indels 2
                                    The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences.
SEQ ID No 52928; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein sequence SEQ ID NO:18473,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        327 KYWEMQPATFRCVLSRMSVQLGNFGM 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 KYWEMQPATFRCVLSRMSVQLGNFGM 379
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nes 305; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB95678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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The present invention describes primer sets for synthasising Soul (2011) length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary trand of a polymucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polymucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polymucleotide which comprises a 3'-end sequence complementary to a polymucleotide which comprises a 3'-end sequence complementary to a polymucleotide which comprises a 3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in gene therapy. The primers are useful for synthesising polymucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the control and/or diagnosis of the abnormality of the full-length cDNAs. The primers are also useful for the control and/or diagnosis of the abnormality of the full-length cDNAs easily without any specialised methods. AAH03165 to AAH13628 and AAH13633 to AAH13633 to AAH13632 to AAH13632 represent human anino acid sequences; and AAH13629 to AAH13632 represent human anino acid sequences; and the exemplification
                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KENDFKGLTSLYGLILUNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTREPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEI 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 KENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDT----DDDDDDDDDDDDDDDDDSDRF 56
                                                                                                                                                                                                                         Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes primer sets for synthesising 5602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.1%; Score 1237; DB 22; Length 246; 96.7%; Pred. No. 5.4e-107; Live 1; Mismatches 3; Indels 4
                                                                                                                                                                                                                       Saito K, Ya
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; SEQ ID 18473; 2537pp + CD ROM; English
                                                                                                                                                                                                                                           Nagai K,
                                                                                                                                                                                                                  Hayashi K,
A, Nagai K,
                                                                                                                                                                                                                                           Wakamatsu
                                                                                                                                                                                                                     Nishikawa T,
                                                                                   2000JP-0118776.
2000JP-0183767.
28-JUL-2000; 2000EP-0116126.
                                           99JP-0248036.
                                                                                                                                 09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the present invention.
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                                                                                                                                                                            (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                         Sugiyama T,
                                                                                                                                                                                                                                                                                    WPI; 2001-318749/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 AA;
                                                                                                                                                                                                                                                                                                                                                                                               full-length cDNAs
                                                                                                                                                                                                                       Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 DNLPS 245
                                                          27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 GLPPT 241
                                           29-JUL-1999:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 237;
                                                                                                                                                                                                                                         Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                     Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57
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QQ
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RESULT 11

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170 NRIRKVPKGVFSGLRNMNCIEMGGNPLENSGFEPGAFDGLKLNYLRISEAKLTGIPKDLP 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB85043 standard; Protein; 368 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human biglycan protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UYBR-) UNIV BROWN RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-NOV-2000; 2000WO-US31661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0166253
                                                                                                                                                                                                                                                             PATFRCVLSRMSVQLGNF 377
                                                                                                                                                                                                                                                                                        350 PATFRCVTDRLAIQFGNY 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-355617/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAF83977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200136475-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB85043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biglycan
                                                                                                                                                         300
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                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurotrophic activity for brain neurons. Recombinant biglycan, obtd. by expression of encoding cDNA (AAT08768) in eukaryotic host cells, can be used to enhance the survival and maintain the structure and function of CNS neurons during normal ageing as well as after pathological and/or traumatic nervous system damage. It can also be used to restore function following nervous system lesions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 -----FSAMCPFGCHCHLRVVQCSDLGLKTVPKEISPDTTLLDLQNNDISELRKD 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 EPRSHFFPFDLFPMCPFGCOCYSRVVHCSDLGLTSVPTNIPFDTRMLDLONNKIKEIKEN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 DFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 DFKGLQHLYALVLVNNKISKIHEKAFSPLRKLQKLYISKNHLVEIPPNLPSSLVELRIHD 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 NKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLP 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              degenerative diseases, and to improve learning efficiency and memory in the elderly and in patients with dementia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 YVLLLFLALCSAKPF----FSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDTR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat biglycan (AAR87951) is a chondroitin sulphate proteoglycan with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biglycan; proteoglycan; chondroitin sulphate; neuron protection; neurotrophic; central nervous system; CNS; memory loss; dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proteoglycan cpds., partic. chondroitin sulphate proteoglycan(s) for maintain structural and function of the CNS and attenuating memory deficit(s) in the elderly and patients with dementia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Koops A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.2%; Score 1040.5; DB 16;
52.6%; Pred. No. 2e-88;
tive 67; Mismatches 93; Ir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Huston J, Junghans U, Kappler J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Hypervariable_region
                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 44-45; 60pp; English.
                          AAR87951 standard; Protein; 369 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BOEF ) BOEHRINGER MANNHEIM GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94WO-EP01479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94WO-EP01479.
                                                                                                                              20-MAR-1996 (first entry)
                                                                                                                                                                               Rat neurotrophic biglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAT08768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hasenoehrl R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9530432-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mueller HW
                                                                                                                                                                                                                                                                                                                                      Rattus sp.
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                                                                              AAR87951;
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                                                                                                                                                                                                                                                                                     learning
                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
AAR87951
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The invention relates to stabilizing dystrophin-associated protein complexes (DAPCs) on the surface of a cell or activating a postsynaptic membrane of a cell that comprises contacting the cell with an effective amount of biglycan. A composition comprising biglycan or its portion DAPC in cells, characterized by breakdown of muscle cell membrane, phore in cells, characterized by breakdown of muscle cell membrane, which includes muscular dystrophies, such as Duchenne's, Becker's, Congenital, Limb-girdle muscular dystrophy and mytonic dystrophy and a condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dystrophin-associated protein complex; DAPC; postsynaptic membrane; biglycan; muscular dystrophy; neuromuscular; neurological; smooth muscle; nootropic; neuroleptic; antiviral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               characterized by abnormal neuromuscular junction or synapse, such as enteromuscular or neurological diseases in a subject. Neurological diseases in a subject. Neurological diseases, include polymyositis and Alzheimer's disease. Biglycan is also useful for preventing and treating smooth muscle disorders, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiac myopathies and for treating and inhibiting infections of cells by microorganisms e.g. viruses. Agents that modulate the activity of DAG-125, identified by the methods are useful in the prophylactic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    postsynaptic membrane of a cell for treating or preventing muscular, neuromuscular and neurological disorders, involves contacting cell with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unstable DAPC or an inappropriate formation of a postsynaptic differentiation. Bigiycans are also useful as a supplement to brain or muscle cell or tissue culture and tissues can be incubated in vitro with biglycan to reverse tissue atrophy and to improve their growth or
                                                                                                           240 PILLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNK 299
                       LKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQ 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapeutic treatments of diseases or disorders, characterized by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stabilizing dystrophin-associated protein complexes and activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Я;
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3,
survival in vitro. The present sequence represents the human biglycan.
                                                                                                                                                  122 KGLTSLYGLILUNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENK 181
                                                                                                                                                                                             62 RSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDF 121
                                                                                                                                                                                                                                                                         242 LLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLK 301
                                                                                                                                                                                                                                                                                                                    KIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPA 361
                                                                     Gaps
                                                                                        7 LVSLLALSQALPFEQRGFWDFTLDDGPFMMNDEEASGADTSGVLDPD-----SVTPTYS-
                                                                                                                                                                                                                            182 VKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurotrophic; central nervous system; CNS; memory loss; dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biglycan; proteoglycan; chondroitin sulphate; neuron protection;
                                                                    20;
                                             Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Koops A;
                                                                  93; Indels
                                            51.9%; Score 1034; DB 22;
53.2%; Pred. No. 8e-88;
iive 63; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kappler J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44..60
/label= Hypervariable_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR87952 standard; Protein; 369 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BOEF ) BOEHRINGER MANNHEIM GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human neurotrophic biglycan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94WO-EP01479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                200; Conservative
                                                                                                                                                                                                                                                                                                                                                                  362 TFRCVLSRMSVQLGNF 377
                                                                                                                                                                                                                                                                                                                                                                                       351 TFRCVTDRLAIQFGNY 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hasenoehrl R, Huston J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-403938/51.
                                                       Best Local Similarity
                      368 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9530432-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mueller HW;
                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR87952;
                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Learning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                Matches
                                                                                                                                                          61
                                                                                                                                                                                                                                                                                              231
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                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
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Human biglycan (AAR87952) is a chondroitin sulphate proteoglycan with neutrotrophic activity for brain neutrons. It can be used to enhance the survival and maintain the structure and function of CNS neurons during normal ageing as well as after pathological and/or traumatic nervous system damage. It can also be used to restore function following nervous system lesions and degenerative diseases, and to improve learning efficiency and memory in the elderly and in patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 IRKVPKGVFSGLRNMNCIEMGGNPLENSGFEPGAFDGLKLNYLRISEAKLTGIPKDLPET 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 LLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 RVPAGLPDLKLLQVVYLHSNNITKVGVNDFCPNGFGVRAYYNGISLFNNPVPYWEVQPA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 ------AMCPFGCHCRLRVVQCSDLGLKSVPKEISPDTTLLDLQNNDISELRKDDF 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 INELHIDHNKIQAIELEDLLRYSKLYRLGLGHNQIRMIENGSLSFLPTLRELHLDNNKLS 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 302 KIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 RSHFFFFFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 KGLTSLYGLILNNNKLTKIHPRAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 LLLFLALCSAKPF----FSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDFPTREP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 LVSLLALSQALPFEQRGFWDFTLDDGPFMMNDEEASGADTTSGVLDPD----SVTPTYS- 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fibromodulin; Decorin; Biglycan; Proteoglycan; Extracellular matrix;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGF-beta; Transforming growth factor-beta; Burn; Wound; Cytostatic; Nephrotropic; Antirheumatic; Antiarthritic; Vasotropic; Vulnerary Antiarteriosclerotic; Hepatotropic; Cardiant; Dermatological; Glomerulonephritis; Rheumatoid arthritis; Arteriosclerosis; Adult respiratory distress syndrome; Cirrhosis; Cancer; Fibrotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 VKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPT
              Proteoglycan cpds., partic. chondroitin sulphate proteoglycan(s) for maintain structural and function of the CNS and attenuating memory deficit(s) in the elderly and patients with dementia
                                                                                                                                                                                                                                                                                                                                                                                                               DB 16; Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             51.8%; Score 1031.5; DB 52.9%; Pred. No. 1.4e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          64; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human biglycan amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG78510 standard; protein; 368 AA.
                                                                                                            Claim 3; Fig 8; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 TFRCVLSRMSVQLGNF 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     352 TFRCVTDRLAIQFGNY 367
                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                 369 AA;
                                                                                                                                                                                                                                                                                                                      with dementia.
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                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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The invention relates to the inhibition of transforming growth factor-beta (TGF-beta) activity involving contacting TGF-beta with a purified polypeptide comprising laucine-rich amino acid sequence of a member of decorin superfamily of mammelian proteoglycans. The following activities can be attributed to the polypeptide of the invention: cytostatic, nephrotropic, antirheumatic, antirarthritic, vasorropic, antiarteriosclerotic, hepatotropic, cardiant, dermatological and valnerary. Polypeptides of the invention act as transforming growth factor-beta (TGF-beta) binder. The polypeptides of the invention can be used for treating a pathology, particularly proliferative pathology caused by a transforming growth factor-beta (TGF-beta) regulated activity such as cancer; particularly fibrotic cancer, fibrotic activity such as cancer; particularly fibrotic activity such as cancer; particularly fibrotic adult respiratory distress syndrome, cirrhosis of liver, fibrosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          other invasive skin injuries and reconstructive surgery. The wounds treated with the polypeptide, particularly decorin exhibit no detectable scarring, and are histologically normal. The current sequence represents
                                                                                                                                                                                                                                                                                                                            decorin or biglycan polypeptide for inhibiting TGF-beta activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lungs, post-myocardial infarction, cardiac fibrosis, post-angioplasty restenosis, renal interstitial fibrosis and certain dermal fibrotic conditions such as keloids and scarring resulting from burn injuries;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 RSHFFFFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ------AMCPFGCHCHLRVVQCSDLGLKSVPKEISPDTTLLDLQNNDISELRKDDF 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.3%; Score 1021; DB 22; Length 368; 52.4%; Pred. No. 1.3e-86;
                                                                                                                                                                                                                                                                                                                                                 in the treatment of dermal wounds and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Pred. No. 1.36
64; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       Example 7; Fig 11; 40pp; English.
                                                                           92US-0978931.
94US-0303238.
88US-0212702.
                  95US-0458834
                                                          91US-0792192
                                                                                                                                      90US-0467888
                                                                                                                                                             92US-0882345
                                                                                                                                                                                                                                            Ruoslahti EI, Yamaquchi Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 197; Conservative
                                                                                                                                                                                                    (BURN-) BURNHAM INST
                                                                                                                                                                                                                                                                                  WPI; 2001-610491/70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human biglycan.
                  02-JUN-1995;
                                                                                              08-SEP-1994;
                                                                                                                                                             13-MAY-1992;
                                                          14-NOV-1991;
                                                                                                                                        22-JAN-1990;
                                                                             17-NOV-1992
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Proteins may also be used to induce or block biological function. (Note: Revised entry submitted to correct the patent number format of US Government-owned NITS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 LVSLLALSQALPFEQRGFWDFTLDDGPFMMNDEEASGADTSGVLDPD----SVTPTYS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probes and Abs raised to the proteins can be used to determine their levels useful in diagnosis of associated concetture fissue diseases states such as osteoporosis, osteo/rheumatoid arthritis, paget's disease, artherosclerosis and periodontal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                                     atherosclerosis; períodontal; human bone matrix; proteoglycan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human bone matrix DNA and proteins - used in detection, diagnosis and treatment involving skeletal and/or connective tissue disease states.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.2%; Score 1020; DB 11; Length 368; 52.1%; Pred. No. 1.6e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              web site at www.derwent.com/dwpi/updates/ntis_us.html.)
                                                                                                                                                                                                                                                        Paget's disease;
                                                                                                                                                                                                                       Sequence of human bone proteoglycan I (biglycan).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66; Mismatches
                                                                                                                                                                                                                                                        Osteoporosis; rheumatoid arthritis;
                                                                                                           AAR05159 standard; protein; 368 AA.
                                                                                                                                                                                                                                                                                                                                                                                                 89US-0432044.
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                                                                                                                                                                           (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (USSH ) NAT INST OF HEALTH
                 351 TFRCVTDRLAIQFGNY 366
362 TFRCVLSRMSVQLGNF 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; ; p; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1990-178641/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ04490.
                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                        09-0CT-1990
                                                                                                                                                                        17-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                  17-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Termine J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                          AAR05159;
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                                                                              RESULT 15
                                                                                           AAR05159
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Bovine biglycan (AAR87953) is a chondroitin sulphate proteoglycan with
                231 LNELHLDHNKIQAIELEDLLRYSKLYRLGLGHNQIRMIENGSLSFLPTLRELHLDNNKLA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurotrophic activity for brain neurons. It can be used to enhance the survival and maintain the structure and function of CNS neurons during normal ageing as well as after pathological and/or traumatic nervous system damage. It can also be used to restore function following nervous system lesions and degenerative diseases, and to improve learning efficiency and memory in the elderly and in patients
                                                                           302 KIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPA 361
242 LLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLK 301
                                                                                                                                                                                                                                                                                                                                                                      neurotrophic; central nervous system; CNS; memory loss; dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteoglycan cpds., partic. chondroitin sulphate proteoglycan(s) for maintain structural and function of the CNS and attenuating memory deficit(s) in the elderly and patients with dementia
                                                                                                                                                                                                                                                                                                                                                      Biglycan; proteoglycan; chondroitin sulphate; neuron protection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Koops A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Huston J, Junghans U, Kappler J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Hypervariable_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                             AAR87953 standard; Protein; 332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BOEF ) BOEHRINGER MANNHEIM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Fig 8; 60pp; English.
                                                                                                                                                                                                                                                                                                                         Bovine neurotrophic biglycan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94WO-EP01479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94WO-EP01479
                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                          351 TFRCVTDRLAIQFGNY 366
                                                                                                                          362 TFRCVLSRMSVQLGNF 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-403938/51,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hasenoehrl R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               with dementia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9530432-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-MAY-1994;
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                                                                                                                                                                                                                                                                                            20-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mueller HW;
                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus
                                                                                                                                                                                                                                                              AAR87953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                    RESULT 16
                                                                                                                                                                                                                  AAR87953
                                                                                      DP
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                             Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang D;
               253 STVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSGLPELKY 312
133 NNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKG 192
                                                                                                                                                                LQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSV 372
                                                                                                                                                                              peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; heamostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and polypeptides, useful for treating disorders
                                                      MNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKI
                                                                                                                           Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu C, Asundi V, Chen R, Ma Y,
Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; SEQ ID NO 7068; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    such as central nervous system injuries
                                                                                                                                                                                                                                                                                                                  AAM42137 standard; Protein; 197 AA.
                                                                                                                                                                                                                                                                                                                                                                                                  Human polypeptide SEQ ID NO 7068.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0727344
                                                                                                                                                                                                                                                                                                                                                                       22-OCT-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAI61293
                                                                                                                                                                                                                                             326 QFGNY 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200153312-A1
                                                                                                                                                                                                                     373 QLGNF 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leukaemia.
                                                                                                                                                                                                                                                                                                                                             AAM42137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhao QA,
                                                                                                                                                                313
                                                                                                                                                                                                                                                                                        RESULT 17
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Gaps

0

64; Indels

51.0%; Score 1015; DB 16; Length 332; 59.0%; Pred. No. 4.1e-86;

73 MCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLLL 132

61; Mismatches

Matches 180; Conservative

QY Db

Similarity

Query Match Best Local 3

us-09-944-457-2.rag

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in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Albehmer's, Parkinson's disease, Huntingfon's disease, amportrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolytic activity, chemotactic/chemokinetic activity, hemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neglected target tissue antigen; NTTA; autoimmunity; autoimmune response;
                                                                                                                                                                                         The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Administration of neglected target tissue antigens to modulate immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 REPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIH 178
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                               1 MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDT - - DDDDDDDDDDDDDDDDDDDDDDFF 58
                                                                                                                                                                                                                                                                                                                                                               3 MKEYVLLLFLALCSARPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDDLSLFPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunotherapeutic agent, insulin dependent diabetes mellitus;
multiple sclerosis; autoimmune thyroiditis; rheumatoid arthritis;
uveoretinitis; inflammatory response.
                                                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                                          50.6%; Score 1007; DB 22; Length 197; 99.0%; Pred. No. 1.1e-85;
                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY57079 standard; protein; 359 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human decorin amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                            Matches 191; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENKVKKIQKDTFK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-052905/04
                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                         197 AA;
                                                                                                                                                                         C.N.S disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2000
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                                                                                                                                                                                                                                             Sequence
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tissue antigens NTTAs are antigens (whole antigens or fragments)

tissue antigens NTTAs. NTTAs are antigens (whole antigens or fragments)

to tinvolved in autoimmunity. These peptides and proteins are used in the invention which involves and mistering an NTTA as an antigen based immunotherapeutic agent, to a host affilicted with an autoimmune disease. The recommenderapeutic agent is used to treat autoimmune diseases such as insulin dependent diabetes mellitus, multiple sclerosis, autoimmune thyroiditis, uveoretinitis, rheumatoid arthritis or abnormal confinamentory inmune responses. The NTTA induces requisitory the NTTA but on participating in the immune response. The NTTA are capable of recognition by substantial populations of uncommitted T cells which can be primed, or biased, towards requisiting undesirable immune tesponses even when target determinants used as agents promoting tolerance agents have failed to induce an effective regulatory T cell response. NTTAs as agents promoting tolerance are anticipated to be safer than use of target determinants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280 KLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFSNPVQYWEI 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequences AAY57063-Y57091 are examples of neglected target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 DFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKEYVLLLFLALCS-AKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDSDNSLFPTR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKATIILLLLAQVSWAGPF---QORGLFDFMLEDEASGIGPEVPDDRD------ 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fibromodulin; Decorin; Biglycan; Proteoglycan; Extracellular matrix;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGF-beta; Transforming growth factor-beta; Burn; Wound; Cytostatic; Nephrotropic; Antirheumatic; Antiarthritic; Vasotropic; Vulnerary Antiarteriosclerotic; Hepatotropic; Cardiant; Dermatological; Glomerulonephritis; Rheumatoid arthritis; Arteriosclerosis; Adult respiratory distress syndrome; Cirrhosis; Cancer; Fibrotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 NKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.4%; Score 963.5; DB 2
50.4%; Pred. No. 2.9e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG78511 standard; protein; 359 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340 QPSTFRCVYVRSAIQLGNY 358
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Matches 191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          359 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Homo sapiens

160 NEITKVRKVTFNGLNOMIVIELGTNPLKSSGIENGAFOGMKKLSYIRIADTNITSIPOGL 219

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factor-beta (TGF-beta) activity involving contacting TGF-beta with a purified polypeptide comprising leucine-rich amino acid sequence of a member of decorin superfamily of mammalian proteoglydans. The following activities can be attributed to the polypeptide of the invention:

Cytostatic, nephrotropic, antirheumatic, antiarthritic, vasotropic, antiarteriosclevotic, hepatotropic, cardiant, dermatological and vulnerary. Polypeptides of the invention act as transforming growth factor-beta (TGF-beta) binder. The polypeptides of the invention can be caused by a transforming growth factor-beta (TGF-beta) regulated activity such as cancer, particularly fibrotic cancer, fibrotic activity such as cancer, particularly fibrotic cancer, fibrotic disease, glomerulonephritis, rheumatoid atthritis, arteriosclerosis, adult respiratory distress syndrome, cirhosis of liver, fibrosis of lungs, post-myocardial infarction, cardiac fibrosis, post-angioplasty restensis, renal interstitial fibrosis and certain dermal fibrotic conditions such as Keloids and scarring resulting ferm burn injuries; other invasive skin injuries and scarring resulting from burn injuries; chemical with the polypeptide, particularly decorin exhibit no detectable scarring, and are histologically normal. The current sequence represents human decorin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of decorin or biglycan polypeptide for inhibiting TGF-beta activity in the treatment of dermal wounds and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 NKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 EPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEN 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.4%; Score 963.5; DB 22; Length 50.4%; Pred. No. 2.9e-81; ive 65; Mismatches 100; Indels
                                                                        /label= Signal_peptide
                      Location/Qualifiers
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94US-0303238.
88US-0212702.
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Best Local Similarity
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22-JAN-1990;
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acquired immunodeficiency virus; dysphagia; gastrointestinal disorder, adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
                               239 PPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENN 298
                                                                                                           299 KLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEM 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     food additive; food preservative; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel central nervous system protein #196.
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                                                                                                                                                                                                                                                       340 QPSTFRCVYVRSAIQLGNY 358
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2000US-0224519.
2000US-0225213.
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2000US-0225268.
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2000US-0205515.
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2000US-0215135.
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14-AUG-2000;
14-AUG-2000;
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19-MAY-2000;
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N-PSDB; ABK43616.
08-NOV-2000;
08-NOV-2000;
17-NOV-2000;
                                                                                                                     17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                 01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                          17-NOV-2000;
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Claim 9; SEQ ID No 804; 837pp; English.

New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -

The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded CC by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include cutoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders c.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. Alzheimer's disease and anglogenesis, nervous system disorders e.g. Alzheimer's disease and amylotrophic lateral sclerosis, infections caused by bacteria, viruses c.g. captured immunodeficiency virus (AIDS) and fungi, ocular disorders c.g. corneal infection, gastrointestinal disorders e.g. dysphagia.

CC agonocarcinomas and irritable bowel syndrome, reproductive system adenocarcinomas and irritable bowel syndrome, reproductive system of storders e.g. testicular femilisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders e.g. nonallergic rhinitis, renal disorders e.g. crepitatory disorders e.g. nonallergic rhinitis, renal disorders e.g. caute kidney failure and blood related disorders e.g. myocardial coult fartion. The polypeptides can also be used to aid wound healing and epitual relations before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,

Page 16

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92US-0865652
                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                     Best Local Similarity 53.9
Matches 178; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mature decorin PT-65.
                                                                                           342 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                    28-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9320202-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-OCT-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                  AAR42260;
                                                                                            Sequence
                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
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                                                                                                                                                                                    109
                                                                                                                                                                                                                                                                            193
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                                                                                                                                                                                                                                                                                                                                  Öλ
                                                                                                                                                                                                                                                                                                                                                   qq
           4
                                                                         PPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENN 298
                                                                                                                                                                                      299 KLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEM 358
                                                                EPRSHFFFFDLFFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEN 119
                                                                                                   120 DFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHE 179
                                                                                                                                       180 NKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGL 238
           Gaps
                           1 MKEYVLLLFFLALCS-AKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDFPTR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exchange resin, a hydrophobic interaction chromatography resin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human recombinant decorin (AAR89439) was obtd. by expression of
          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Purificn. of human recombinant decorin - using a strong anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parker JR;
                                            2 MKATIILLLLAQVSWAGPF---QORGLFDFMLEDEASGIGPEVPDDRD----
          Indels
                                                                                                                                                                                                                                                                                                                                                                                        Decorin; PG-II; PG-40; proteoglycan; guanidinium ion.
Pred. No. 2.9e-81;
5; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kostel PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hernandez SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1A-D; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Sig_peptide
                                                                                                                                                                                                                                                                                                               AAR89439 standard; Protein; 342 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LJOL-) LA JOLLA CANCER RES FOUND,
         65;
                                                                                                                                                                                                                                                            ||:||||| | ::||||:
| QPSTFRCVYVRSAIQLGNY 359
                                                                                                                                                                                                                                                 QPATFRCVLSRMSVQLGNF 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-0272919.
50.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95WO-US08542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                strong anion exchange resin
                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                      Human recombinant decorin.
          191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harper JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-097586/10.
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAT10741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9601842-A1
                                                                                                                                                                                                                                                                                                                                                   20-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craig WS,
Vedvick TS;
                                                                                                                                                                                                                                                                                                                                  AAR89439;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
          Matches
                                                                                 47
                                                                                                                                                         161
                                                                                                                                                                          239
                                                                                                                                                                                                                                                                    341
                                                                                                                                                                                                                                                                                              RESULT 21
                                                                                                                                                                                                                                                                                                         AAR89439
                                                                δy
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                                                                                                   δλ
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                                                                                                                                                                                                              δy
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49 DDEDNSLFPTREPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDL 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288 PRVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAIS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228 EAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANI 287
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 EDEASGIGP-EVPDDRDFEPSLGPYCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDL 72
Decorin (or PGII or PG-40)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leucine-rich repeat; proteoglycan; cell regulatory factor; MBP; fusion protein; maltose binding protein; tumour growth; inhibition; decorin; PG-1I; PG-40; transforming growth factor-beta; TGF-beta.
                  is a proteoglycan having a 40 kba core profein. Recombinant decorin can be produced by cotransfection of CHO-DG44 cells with pSV2-decorin and pSV2dhfr. Large-scale cultures can be performed using CHO cells attached to microcarrier beads. The recombinant protein is purified from the cells using a 3-step chromatographic guanidinium ions (ppm range), partic. in protein-confg. solins. purified using GHC1, and also has therapeutic applies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIA
                                                                                                                                                                                                                                                                                                                                                                                                                  5;
                                                                                                                                                                                                                                                                                                                                                             DB 17; Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46..280
/label= repeat_region
/note= "contains 10 leucine-rich repeats"
281..31
/label= C-terminal_region
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "contains 4 Cys residues"
                                                                                                                                                                                                                                                                                                                                                       47.6%; Score 949; DB 17; 53.9%; Pred. No. 6.1e-80; ive 63; Mismatches 87.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= N-terminal_region
cDNA clone (AAT10741) in CHO host cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 LFSNPVQYWEIQPSTFRCVYVRSAIQLGNY 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFNNPVKYWEMQPATFRCVLSRMSVQLGNF 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR42260 standard; Protein; 331 AA
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Sequence
   Domain
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AAY84539
   qq
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                                                                                                                                                                                                                                 7
                                                                                                                                                                                                                                                50 DEDNSLFPTREPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQ 109
                                                                                                                                                                                                                                                                                                                                                           229 AKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIP 288
                                                                                                                                                                                                                                                                                                                                                                                241
                                                                                                                                                                                                                                                                                                                                                                                                289 RVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISL 348
                                                                                                                                                                                                                                                                                     110 NNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLP 169
                                                                                                                                                                                                                                                                                               Active fragments of decorin (full-length coding sequence AAQ50046) were generated by PCR and fused to Maltose Binding Protein. The resulting fusion proteins were useful for inhibiting the activity of a cell regulatory factor, esp. IGF-beta, and hence for treating conditions associated with over-activity of the growth factor such
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                          Transforming growth factor; TGF-beta-1; collagen IA; osteogenesis;
                                                                                                                                                                                                                                                                                                                        170 KSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAE
                                                                     Active fragments of protein esp. decorin - with cell regulatory factor domain, useful for inhibiting cell regulatory factor
                                                                                                                                                                                                                                 2,
                                                                                                                                                                                                              Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Collagen-IA
/note= "collagen IA alpha-helical domain"
                                                                                                                                                                                                                                Indels
                   Pierschbacher MD;
                                                                                                                                                                                                           47.5%; Score 947; DB 14;
54.1%; Pred. No. 8.9e-80;
Live 62; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bone formation; tissue repair; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                             1058..1059
/label= Linker_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                    349 FNNPVKYWEMQPATFRCVLSRMSVQLGNF 377
                                                                                                         Claim 10; Page 36-38; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR89471 standard; Protein; 1388 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                  Mullen DG,
(LJOL-) LA JOLLA CANCER RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collagen/decorin fusion protein.
                                                                                                                                                                                                                     54.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                               Matches 178; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..1057
                   Craig W,
                                           WPI; 1993-336910/42.
                                                                                                                                                                                                                     Sest Local Similarity
                                                                                                                                                                        as certain tumours
                                                                                                                                                                                           331 AA;
                                                     N-PSDB; AAQ50046
                         Ruoslahti EI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996
                  Cardenas J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                           Sequence
                                                                                         activity
                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR89471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289 RVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISL 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 DEDNSLFPTREPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human colfagen I(a) linked, compressed in Escherichia coli transformants decorin). It can be expressed in Escherichia coli transformants carrying a vector incorporating a chimeric gene (AAT16517) coding fit the fusion. The decorin binds to type I collagen and thus affects Elbril formation. It inhibits the cell attachment-promoting activity of collagen and fibrinogen by binding to such molecules near their cell binding sites. The collagen moiety provides an integral substratum or scaffolding for the decorin. The fusion protein acts to reduce scarring of healing tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimaeric DNA encoding protein contg. extracellular matrix protein domain - and cellular regulatory factor domain, partic. useful as osteogenic agents, also related vectors, transformed cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 NNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 KSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A fusion protein (AAR89471) comprises the alpha-helical region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2,
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                                                                                                                                                                           /note= "unidentified amino acid"
                                                                                                                                                                                                                                                                                         /note= "unidentified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.5%; Score 947; DB 17; 54.1%; Pred. No. 6.6e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FNNPVKYWEMQPATFRCVLSRMSVQLGNF 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 7; 59pp; English.
1060..1388
/label= Decorin
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Best Local Similarity 54.18
Matches 178; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSU ) US SURGICAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gruskin EA;
                                                                                                                    887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-140144/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1388 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chimaeric proteins
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                                                                                                                    Misc-difference
                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .0-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                             CA2151547-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Espino P,
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Claim 25; Fig 17A-B; 260pp; English.
                                                                                        Location/Qualifiers
                                                                                                                                    'note= "Glu encoded
                                                                                                                                                                     /note= "Gly encoded
AAY84539 standard; Protein; 1388
                                                                                                                                                                                                                                                                          99EP-0119184
                                                                                                                                                                                                                                                                                     98US-0169768
                                                                                                                                                                                                                                                                                                            Buechter DD,
                      (first entry)
                                                                                                                                                                                                                                                                                                 (USSU ) US SURGICAL CORP
                                                                        Chimeric - Homo sapiens.
Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                       WPI; 2000-259138/23.
                                                                                                                     Misc-difference 363
                                                             chimera.
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                                                                                                         Misc-difference
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                                                                                                                                                                                                                                                                          07-OCT-1999;
                                                                                                                                                                                                                                                                                     09-0CT-1998;
                                                                                                                                                                                                                                                                                                            Gruskin EA,
                      25-JUL-2000
                                                                                                                                                                                                                                                    EP992586-A2
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           AAY84539;
                                                              decorin;
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FNNPVKYWEMQPATFRCVLSRMSVQLGNF 377
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                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                               1388 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-NOV-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-APR-1990.
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                                                                                                                                                                                                                                                                             Matches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Termine J;
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                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δλ
                                                                                                                                               trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily hydroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell; incorporating the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino
                                                                                                Amino acid sequence of a chimeric collagen 1 (alphal)/decorin protein.
                                                                                                                                 Extracellular matrix protein; self aggregation; hydroxylated proline;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The specification describes a method for producing an extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Production of extracellular matrix proteins containing
4-trans-hydroxyproline results in native self aggregating proteins,
useful on medical implants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang G, Connolly K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by CTT"
                                                                                                                                                                                                                                                                                                                                 'note= "Glu encoded by CAA"
                                                                                                                                                                                                                                                                                                                                                                                                 by GGT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "Gly encoded by CGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "Gly encoded by GCT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 by CGT"
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                                                                                                                                                                                                                                                                                                'note= "Gly encoded by GCG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                by CGA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Gly encoded
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   AA.
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                                                                                                                                                  incorporate trans-4 hydroxyproline into proteins. This is especially useful in the recombinant production of proteins such as collagen, fibrinospen and fibronectin whose ability to self aggregate and produce functional proteins depends on the post translational hydroxylation of proline. The method is also useful in studying the structure and function of polypeptides which do not normally contrain trans-4-hydroxyproline. The present sequence represents a chimneric collagen I (alphal)/decorin protein, which may be produced using the method of the invention.
acid, selected from the group consisting of trans-4-hydroxyproline and 3-hydroxyproline to allow at least one of the amino acids to be assimilated into the cell and incorporated into the extracellular matrix protein. The method may be used to make host cells assimilate and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1299 HLRELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSL 1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289 RVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISL 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 DEDNSLFPTREPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 NNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLP 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 AKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIP 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 KSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atherosclerosis; periodontal; human bone matrix; proteoglycan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.5%; Score 947; DB 21; Length 1388; 54.1%; Pred. No. 6.6e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Osteoporosis; rheumatoid arthritis; Paget's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence of human bone proteoglycan II (decorin).
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92US-0865652
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302 FSNP 305
                                                Cardenas J, (
Ruoslahti EI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349 FNNP 352
    03-APR-1992;
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                                                                                                                                                                                                                                                                                                                       162;
                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                           activity
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                                                                                                                                                                                                                                                                                                              Local
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                                                                                                   their levels useful in diagnosis of associated conective tissue diseases states such as osteoporosis, osteo/rhemmatoid arthritis, Paget's disease, artherosclerosis and periodontal disease.

Proteins may also be used to induce or block biological function. (Note: Revised entry submitted to correct the patent number format of US Government-owned NITS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent web site at www.derwent.com/dwpi/updates/ntis_us.html.)
                                                                                                                                                                                                                                                                                                                                                                                                                                       66 FPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLT 125
                                                                                                                                                                                                                                                                                                                                                                                         280 GGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFSNPVQYWEIQPSTFR 339
                                                                                                                                                                                                                                                                                                                                                                             SLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKI 185
                                                                                                                                                                                                                                                                                                                                                                                                                         186 QKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGLPPTLLE 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 LHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIP 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFR 364
                                                                                                                                                                                                                                                                                  LLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDDDDDFPRSHF 65
                                                                                                                                                                                                                                                                                                        1 LLLLAQVSWAGPF---QQRGLFDFMLEDEASGIGPEVPDDRD-------39
                                                                                                                                                                                                                                                                                                                                           leucine-rich repeat; proteoglycan; cell regulatory factor; MBP;
fusion protein; maltose binding protein; tumour growth; inhibition;
decorin; PG-II; PG-40; transforming growth factor-beta; TGF-beta.
                                                                                                                                                                                                                                                            22;
                                                                                            Probes and Abs raised to the proteins can be used to determine
                                  used in detection, diagnosis and treatment involving skeletal and/or connective tissue disease states.
                                                                                                                                                                                                                                      Length 353;
                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Decorin sequence PT-78 (N-terminal to half C-terminal).
                                                                                                                                                                                                                                   45.5%; Score 907; DB 11;
49.1%; Pred. No. 5.2e-76;
tive 61; Mismatches 107;
                        Human bone matrix DNA and proteins -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR42267 standard; Protein; 305 AA
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                                                                                                                                                                                                                                                          Matches 183; Conservative
                                                                     Disclosure; ; p; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340 CVYVRSAIQLGNY 352
                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                             353 AA;
 N-PSDB; AAQ04491
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                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                            126
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DEDNSLFPTREPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQ 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 RVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISL 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 KSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAE 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 AKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIP 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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stem cell proliferation, haematopoiesis, nerve tissue regeneration;
immune suppression, immune stimulation, anti-inflammatory, leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     were generated by PCR and fused to Maltose Binding Protein. The resulting fusion proteins were useful for inhibiting the activity of a cell regulatory factor, esp. TGF-beta, and hence for treating conditions associated with over-activity of the growth factor such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Active fragments of decorin (full-length coding sequence AAQ50046)
                                                                                                                                                                                                                                             fragments of protein esp. decorin - with cell regulatory domain, useful for inhibiting cell regulatory factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.5%; Score 847; DB 14; Length 305; llarity 53.3%; Pred. No. 1.7e-70; Conservative 56; Mismatches 84; Indels
                                                            Mullen DG, Pierschbacher MD;
                                                                                                                                                                                                                                                                                                                                                               Claim 10; Page 49-50; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU30348 standard; Protein; 423 AA.
(LJOL-) LA JOLLA CANCER RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human secreted protein #839.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                               Craig W,
                                                                                                                                                 WPI; 1993-336910/42.
N-PSDB; AAQ50053.
                                                                                                                                                                                                                                             Active fragments of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as certain tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 AA;
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RESULT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
                                                                                                                                                                                                                                      polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically the proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to
                                                                                                                                                                                                                                                                                                                                                                                       increase stem cell proliferation; to regulate haematopolesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU39510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.
                                                                                                                                                          Nucleic acids encoding a range of hu\mathrm{man} polypeptides, useful in genetic vaccination, testing and therapy ^{\text{-}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 RSHFFFFDLFPMCPFGCQCYSRVVHCS-DLGLTSVPTNIPFDTRMLDLQNNKIKEIKEND 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -------AMCPFGCHCHLRVVQCAPTLGLKSVPKEISPDTTLLDLQNNDISELRKDD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 FKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHEN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 KVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV----TVFHIRIAEAKLTS-VP 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGLPPTLLELHLDYNKISTVEL-EDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIH 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 KYLPETLNELHLDHNKIQGHRTGRDLLRYSKLYRLGLGHNQIRMIENGSLSFLPTLREVH 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENNKLKKIPSGLPELKYLQIIF-LHSNSIARVGV-NDFC------PTVPKMKKSL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 LVSLLALSQALPFEQRGFWDFTLDDGPFMMNDEEASGADTSGVLDPD----SVTPTYS-
                                                                                                                                                                                                                              The invention relates to novel human secreted polypeptides. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.8%; Score 793.5; DB 2: 45.8%; Pred. No. 2.6e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343 YSAISLFN-NPVKYWE-MQPATFRCVLSRMSVQLG 375
                                                                                                                                                                                                   Claim 20; Page 281; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR42266 standard; Protein; 280 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60;
                                                                                                         Tang YT, Liu C, Drmanac RT;
            16-APR-2001; 2001WO-US08656.
                                    2000US-0552929.
2001US-0770160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 181; Conservative
                                                                                                                                 WPI; 2001-611725/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          423 AA;
                                                                              (HYSE-) HYSEQ INC.
                                    18-APR-2000;
26-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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ID AAR4
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50 DEDNSLEPTREPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQ 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 AKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIP 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 TNITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTP 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Active fragments of decorin (full-length coding sequence AAQ50046) were generated by PCR and fused to Maltose Binding Protein. The resulting fusion proteins were useful for inhibiting the activity of a cell regulatory factor. esp. GPF-beta, and hence for treating conditions associated with over-activity of the growth factor such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                      fusion protein; maltose binding protein; tumour growth; inhibition; decorin; PG-II; PG-40; transforming growth factor-beta; TGF-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 DEASGIGP-EVPDDRDFEPSLGPVCPFRCQCHIRVVQCSDLGLDKVPRDLPPDTTLLDLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 NNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLP
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                                                                                                                                                                                .eucine-rich repeat; proteoglycan; cell regulatory factor; MBP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Active fragments of protein esp. decorin - with cell regulatory factor domain, useful for inhibiting cell regulatory factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craig W, Mullen DG, Pierschbacher MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 HLRELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVG 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 RVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIARVG 327
                                                                                                                   Decorin sequence PT-77 (N-terminal to LRR10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 10; Page 47-48; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (LJOL-) LA JOLLA CANCER RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU20404 standard; Protein; 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92US-0865652.
                                                                                                                                                                                                                                                                                                                                                                                                                             93WO-US03171.
                                                         (first entry)
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Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-336910/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               certain tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ50052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cardenas J, (
Ruoslahti EI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-APR-1992;
                                                         28-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                 02-APR-1993;
                                                                                                                                                                                                                                                                                                             WO9320202-A.
                                                                                                                                                                                                                                                                                                                                                                    14-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU20404;
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AAR42266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activity
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Immunomodulatory; human immunodeficiency virus; HIV; anaemia; angina; rhemmatoid arthritis; antiarteriosclerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial; ophthalmological; cytostatic; Alzheimer's disease; Parkinson's disease; human; cancer; multiple sclerosis; cancer; hyperproliferative disorder; infection; Gaucher's disease; neurological disease; cerebrovascular disorder;
              Human secreted protein, Seg ID No 396.
06-DEC-2001 (first entry)
                                                               thrombosis; wound healing.
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Homo sapiens.

WO200155326-A2

02-AUG-2001.

17-JAN-2001; 2001WO-US01347.

31-JAN-2000; 2000US-0179065.

(HUMA-) HUMAN GENOME SCI INC

Barash SC, Ruben SM; Rosen CA,

WPI; 2001-451931/48. N-PSDB; AAS33113 New nucleic acids and polypeptides, useful for diagnosing, preventing or treating medical conditions -

Claim 11; SEQ ID No 396; 753pp; English.

The INVELLOR TELATES to novel 1801ated nucleic acid molecules (1) and coling human secreted proteins (11). (1) and (11) are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, agoats, cats, dags, chickens or sheep. (1) and (11) may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate expression of secreted proteins. (1) and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (FCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples, and so which patients may the production of antibodies and in assays to identify modulators and the production of antibodies and natagonists may also be used to down requiate expression and activity of the secreted proteins. The anti-(11) antibodies and antagonists may also be used to down requiate expression and activity of (11). The anti-(11) antibodies and antagonists may also be used as diagnostic agents for (11). The anti-(11) antibodies of an ununosorbant assay (EIISA). The disorders include for example: immune/autorimmune diseases (e.g. HIV) (human immunodeficiency virus) infections, anaemia, rheumatorid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. parkinson's disease), neurological diseases (e.g. Alzheimer's disease, cerebrovascular disorders (e.g. cardiac arrest, tachycardia, viruses and charcot-Marie-Tooth disease), cardio-/candiar disorders (e.g. cardiac arrest, tachycardia, and and antibodies can also be used to promote wound healing, maintain organs before transplantation, and support cell culture of primary tissues. AAUJ0342-AAUZ066 repersent human servet arrest or primary experience of primary contract and antibodies can also be used to promote voreice of primary tissues. of primary tissues. AAU20342-AAU20666 represent human secreted protein amino acid sequences, and related sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification but was obtained in electronic format directly from WIPO invention relates to novel isolated nucleic acid molecules (I) at: ftp.wipo.int/pub/published\_pct\_sequences.

Seguence

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0
                        Gaps
                         .;
0
   Length 128;
                         Indels
 Score 643; DB 22;
Pred. No. 5.2e-52;
0; Mismatches 2;
32.3%;
                    Matches 125; Conservative
Query Match
Best Local Similarity
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253 STVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSGLPELKY 312
                                                           313 LQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSV 372
                                                                             110 NNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLP 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 NNKITEIKDGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 KSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAE 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 DEDNSLFPTREPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQ 109
                  2 STVELEDXKRXKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSGLPELKY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Active fragments of decorin (full-length coding sequence AAQ50046) were generated by PCR and fused to Maltose Binding Protein. The resulting fusion proteins were useful for inhibiting the activity of a cell regulatory factor. esp. IGF-beta, and hence for treating conditions associated with over-activity of the growth factor such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         leucine-rich repeat; proteoglycan; cell regulatory factor; MBP; fusion protein; maltose binding protein; tumour growth; inhibition; decorin; PG-II; PG-40; transforming growth factor-beta; TGF-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fragments of protein esp. decorin - with cell regulatory domain, useful for inhibiting cell regulatory factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.9%; Score 616; DB 14; Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craig W, Mullen DG, Pierschbacher MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 4e-49;
                                                                                                                                                                                                                                                                                                                                  Decorin sequence PT-76 (N-terminal to LRR8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 10; Page 45-46; 77pp; English.
                                                                                                                                                                                                                                     AAR42265 standard; Protein; 234 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LJOL-) LA JOLLA CANCER RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93WO-US03171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.48;
                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1993-336910/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Active fragments of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as certain tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ50051.
                                                                                                                          373 QLGNFGM 379
                                                                                                                                                        122 QLGNFGM 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruoslahti EI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cardenas J,
                                                                                                                                                                                                                                                                                                                                                                                                                               W09320202-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Sim
                                                                                                                                                                                                                                                                     AAR42265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                      RESULT 30
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δλ qq

AAY64720 standard; Protein; 88 AA.

(first entry)

01-FEB-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs different total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed CDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
229 AKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIEN 281
                                    24.7%; Score 493; DB 21; Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dumas Milne Edwards J, Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 13; SEQ ID 4322; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred. No. 3e-
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein, SEQ ID NO: 4322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRSHFFPFDLFPMCPFGCQCYSRVVHCS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PRSHFFPFDLFPMCPFGCQCXSRVVHCS 88
                                                                                                                                                                                                                          AAG00241 standard; Protein; 88 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-2000; 2000EP-0200610.
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                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Matches 88; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                    06-0CT-2000
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                                                                                                                                                                                                                                                                                     AAG00241;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell. The proteins encoded by the EST sequences may be useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnostic, forensic, gene therapy, and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               secreted proteins is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKEYVLLIFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDDFPTRE 60
                                                                                                                                                                                                                                              Human, 5' EST; expressed sequence tag; secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensic; location; development; protein synthesis; stability;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel secreted protein 5' expressed sequence tag sequences used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treating a variety of human conditions. Secreted proteins have therapeutic value, and the identification of new secreted proteins valuable. AAZ42249 to AAZ4226 and AAY64644 to AAY64650 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.7%; Score 493; DB 21; Length 88; 100.0%; Pred. No. 3e-38; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dumas Milne Edwards J, Duclert A, Giordano J;
                                                                                                                                                                                Human 5' EST related polypeptide SEQ ID NO:881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 621; 837pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-IB00712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0057719
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                                                                                                                                                                                                                                                                                                                                         regulation; identification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPT: 2000-038446/03.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-APR-1999;
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RESULT 32 AAY64720

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This invention describes novel nucleic acid sequences that are highly expressed in normal ovary tissue. Artificial chromosomes and cosmid clones containing the sequences can be used as gene transfer vehicles. The sequences can be used to produce DNA fragments containing full-length genes. Host cells transformed with the sequences can be used to produce polypeptides transformed with the sequences can be used to screen phage displays for polypeptide fragments, which can be used to screen phage displays for polypeptides that bind to them, or as tools for identifying agents active against ovarian cancer, or to prepare medicaments for treating ovarian cancer. The cDNA sequences can be used to obtain genomic genes, their promoters, enhancers, silencers, exon structures, intron structures and their splice variants. AAY59724-Y59837 represent protein fragments encoded by the cDNA sequences represented in AAX41222-Z41324 which are derived from normal human ovarian tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 PPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENN 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 KLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEM 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic, anticheumatic; antiarthritic; antiviral; antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 PPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHLRELHLDNN 66
                                                                                                                                                                                                                                                                                                                                                      Nucleic acid sequences potentially useful in diagnosis or therapy of
                                                                                                                                                                                                                                                                      Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cancer associated protein sequence SEQ ID NO:1561.
                                        Human; ovary; screening; ovarian cancer; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.7%; Score 433; DB 20; 55.4%; Pred. No. 2.4e-32;
     Human normal ovarian tissue derived protein 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28; Mismatches
                                                                                                                                                                                                                                         (META-) METAGEN GES GENOMFORSCHUNG MBH.
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 23; Page 226; 274ppp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            359 QPATFRCVLSRMSVQLGNF 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 QPSTFRCVYVRSAIQLGNY 145
                                                                                                                                                                      98DE-1016395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 AA;
                                                                                                                                                                                                                                                                                                                   N-PSDB; AAZ41234
                                                                                                                                                                                                                                                                                                                                                                         ovarian cancer
                                                                                                    DE19816395-A1
                                                                       Homo sapiens
                                                                                                                                                                      03-APR-1998;
                                                                                                                                     07-0CT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 DEDNSLFPTREPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Active fragments of decorin (full-length coding sequence AAO50046) were generated by PCR and fused to Maltose Binding Protein. The resulting fusion proteins were useful for inhibiting the activity of a cell regulatory factor. esp. TGF-beta, and hence for treating conditions associated with over-activity of the growth factor such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 NNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLP 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 KSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAE 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leucine-rich repeat; proteoglycan; cell regulatory factor; MBP; fusion protein; maltose binding protein; tumour growth; inhibition; decorin; PG-II; PG-40; transforming growth factor-beta; TGF-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Active fragments of protein esp. decorin - with cell regulatory factor domain, useful for inhibiting cell regulatory factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.7%; Score 493; DB 14; Length 186; 53.0%; Pred. No. 8.4e-38; ative 32; Mismatches 53; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                    Craig W, Mullen DG, Pierschbacher MD;
                                                                                                             Decorin sequence PT-75 (N-terminal to LRR6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Page 43-44; 77pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY59749 standard; Protein; 146 AA.
             AAR42264 standard; Protein; 186 AA
                                                                                                                                                                                                                                                                                                                                                 (LJOL-) LA JOLLA CANCER RES FOUND
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                                                                                                                                                                                                                                                                                                                  92US-0865652
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                                                                                28-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                Cardenas J,
Ruoslahti EI;
                                                                                                                                                                                                                                                                                 02-APR-1993;
                                                                                                                                                                                                                                                                                                                  03-APR-1992;
                                                                                                                                                                                                                                                 14-OCT-1993.
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in AAA43398 to AAA4239. The proteins can have activities based on the tissues and calls the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antitherary; immunomodulator; antidiabetic; antibacterial; antibacterial; antibacterial; antibacterial; antibacterial; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antiangiogenic. The polymucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polymucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoletic cells, autoimmune cells, to treat disorders of haematopoletic cells, autoimmune rejection, modulate haemostatic or thrombolytic activity, modulate namostatic or thrombolytic activity, modulate calcinous. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAA44240 represent sequences used in the exemplification of
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dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antianglogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
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                                                                                                                  Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 KOMEDIDDDDDDDDDDDDDDDDDDDDDDL-----PPIREPRSHFFPFDLFP-----MCPFGC 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 HYLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKISTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TDIENGSLANIP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                         physiologically active protein specifically derived from mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.0%; Score 397.5; DB 21; Length 699; 24.9%; Pred. No. 4.3e-28; ive 77; Mismatches 148; Indels 101;
                                                                                                                                     arteriosclerosis; hyperuricemia; sleep apnea syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 24-27; 50pp; Japanese.
                                                                                   Human adipose tissue protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELEDFKRYKELQRLGLGNNKI - - -
                                                                                                                                                                                                                                                                              98JP-0225228.
                                                                                                                                                                                                                                                                                                                   98JP-0225228.
                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 24.9%
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                  (NISB ) JAPAN TOBACCO INC.
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                                                                                                                                                                                                           JP2000037190-A.
                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                23-JUL-1998;
                                                                                                                                                                                                                                                                                                                   23-JUL-1998;
                                                 13-JUN-2000
                                                                                                                                                                                                                                            08-FEB-2000
              AAY67598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
qq
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Db 680 YTFSCIRSYSSIVL 693
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in ABB4338 to AAB44239. The proteins cancer associated proteins given tissues and cells the genes are expressed in. Example of activities based on the tissues and cells the genes are expressed in. Example of activities conclude cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antibarterial; antiviral; antinflammatory; antiphyroid; antialleragic; antibarterial; antiviral; antinflammatory; antiphyroid; antialleragic; antibarterial; antiviral; cartinflammatory; antiphyroid; antialleragic; antibarterial; antiviral; coording and polypeptides can be used for preventing, treating or molynelocides, polypeptides and diagnosing pathological conditions. Polynucleotides, polypeptides and diagnosists and antagonists from the present invention may be used to treat immune disorders by activating immune cells, to treat disorders of haematopolatic cells, autoimmune cells, to treat disorders of haematopolatic cells, autoimmune cellscrib, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and cancers and cancers, cardiovascular disorders, neurological disease and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antiathabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antiinflammatory; antitherent antianthritic; antiviral; antiinflammatory; antithyroid; antiantherapic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coaqulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; hardred; hardred; call disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC77607 to AAC78448 encode the human cancer associated proteins given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acids comprising sequences encoding peptides
                                                                                                                                                                                                                                cancer associated gene; cancer antigen; detection; cancer;
                                                                                                                                                                                     Human cancer associated protein sequence SEQ ID NO:980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for treating or diagnosing e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 1552-1553; 2352pp; English.
                                            AAB43535 standard; Protein; 353 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAR-2000; 2000WO-US05882.
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                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen CA, Ruben SM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens,
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                                                                                                                                        08-FEB-2001
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                                                                                            AAB43535;
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RESULT 37
                         AAB4353
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The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumnour endothelial marker (TEM) protein selected from ABB90732, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antianglogenic activity. They are useful for inhibiting tumour growth, necanglogenesis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic normal endothelial marker; pan-endothelial marker; immunostimulant; antiangiogenic; tumour; neoangiogenesis; vascularised tumour; neoangiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
                                                                               176
                                                                                                 99 KAFENVTDLQWLILDHNLLENSKIKGRVFSKLKQLKKLHINHNNLTESVGPLPKSLEDLQ 158
                                                                                                                                                                                                                                                 216 SGLPVSLLTLYLDNNKISNIPDEXFKRFNALQYLRLSHNELADSGIPGNSFNVSSLVELD 275
66 FPFDLF----PMCPFGCQC---YSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKE 118
                                                                                                                                                  177 IHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVP 235
                                                                                                                                                                                                                           KGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIE-NGSLANIPRVREIH 294
                                                                                                                                                                                                                                                                                                       LENNKLKKIPSGLPELK--YLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNP 352
                                                                                                                                                                                                                                                                                                                                        LSYNKLKNIPTVNENLENYYLEV----NQLEKFDIKSFCKILGPLSYSKIKHLRLDGNR 330
                                         98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth -
                     40 FPLSIYGQSSPNCAPECNCPESYPSAMYCDELKLKSVPM-VPPGIKYLYLRNNQIDHIDE
                                                                         119 NDFKGLTSLYGLILNNNKL--TKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELR
                                                                                                                                                                                        159 LTHNKITKL--GSFEGLVNLTFIHLQHNRLKEDAVS-AAFKGLKSLEYLDLSFNQIARLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Tumour Endothelial Marker polypeptide SEQ ID NO 259.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 54; Page 262-263; 331pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB90763 standard; Protein; 338 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                    331 ISXTSLPPDMYECLRXANEVTL 352
                                                                                                                                                                                                                                                                                                                                                                                353 VKYWEMQPATFRCVLSRMSVQL 374
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2001US-282850P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-291856/33.
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11-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2002
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Gaps

22;

19.7%; Score 393; DB 21; Length 353; 31.7%; Pred. No. 4.3e-28; tive 70; Mismatches 128; Indels 2:

Conservative

102;

Matches

Similarity

Query Match Best Local :

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10;
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            diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075.ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and ABL92143.ABL92191; normal endothelial markers (NEM) ABL92041 and pan-endothelial markers (NEM) ABL91995.
                                                                                                                                                                                                                                                                                                                         201 SGLPVSLLTLYLDNNKISNIPDEYFKRFNALQYLRLSHNELADSGIPGNSFNVSSLVELD 260
                                                                                                                                                                                                                                     66 FPFDLF----PMCPFGCQC---YSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKE 118
                                                                                                                                                                                                                                                                                                       119 NDFKGLTSLYGLILNNNKL--TKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELR 176
                                                                                                                                                                                                                                                                                                                                                                          IHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVP 235
                                                                                                                                                                                                                                                                                                                                                                                                       144 LTHNKITKL--GSFEGLVNLTFIHLOHNRLKEDAVS-AAFKGLKSLEYLDLSFNQIARLP 200
                                                                                                                                                                                                                                                                                                                                                                                                                                          KGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIE-NGSLANIPRVREIH 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENNKLKKIPSGLPELK--YLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNP 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSYNKLKNIPTVNENLENYYLEV ----NOLEKFDIKSFCKILGPLSYSKIKHLRLDGNR 315
subjects bearing a vascularised tumour, polycystic kidney disease,
                                                                                                                                                                                                                                                                    25 FPLSIYGQSSPNCAPECNCPESYPSAMYCDELKLKSVPM-VPPGIKYLYLRNNQIDHIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                     22;
                                                                                                                                                                     Length 338;
                                                                                                                                                                                                     122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human colon cancer antigen protein SEQ ID NO:4645.
                                                                                                                                                                 19.6%; Score 390; DB 23; 31.8%; Pred. No. 7.8e-28; tive 70; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          colorectal carcinoma; chromosome 12.
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99US-0163280.
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                                                                                                                                                                                                       Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               353 VKYWEMQPATFRCV 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 ISETSLPPDMYECL 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-235357/24.
                                                                                                                                                                                      Similarity
                                                                                                                                    338 AA;
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03-NOV-1999;
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                                                                                                                                        Sequence
                                                                                                                                                                      Query Match
                                                                                                                                                                                          Best Local
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the proteins are collectively known as colon cancer associated nucleic acid molecules (N) and proteins. The colon cancer antigens have expostatic activity and cancer antigens. The colon cancer antigens have expostatic activity and cancer antigens. The colon cancer associated with inappropriate P capterssion. For example, N and P may be used to treat disorders cassociated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. additionally, N may be used to produce the colon cancer associated Ps. by inserting the nucleic acids into a host cell and culturing the cell to the activity of patients of the presention. Additionally, and production of the colon cancer associated Ps. and treatment of colorectal carcinomas and cancers. AAH31196 to AAH37204 and AAB37789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 FPFDLF----PMCPFGCQC---YSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKE 118
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Claim 11; Page 6448-6450; 9803pp; English.
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N.B. Pages 666 to 6
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                                                                                                                                                                                                                                                                                                   50 DEDNSLFPTREPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVP1NIPFDTRMLDLQ 109
                                                                                                                                                                                                                                                                                                                                                            62 NNKITEIKDGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNOLKELPEKMP 121
                                                                                                                                                              Active fragments of decorin (full-length coding sequence AAQ50046) were generated by PCR and fused to Maltose Binding Protein. The resulting fusion proteins were useful for inhibiting the activity of a cell regulatory factor. esp. IGF-beta, and hence for treating conditions associated with over-activity of the growth factor such
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                1;
                                                                                                    Active fragments of protein esp. decorin - with cell regulatory factor domain, useful for inhibiting cell regulatory factor
                                                                                                                                                                                                                                                             19.3%; Score 384.5; DB 14; Length 139; 55.1%; Pred. No. 7.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiovascularisation; wound healing; cancer; atherosclerosis;
cardiac hypertrophy; myocardial infarction; antiangiogenic;
antitumour; tissue regeneration; pulmonary fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurological disease; macular degeneration; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goddard A, Gurney AL, Hillan K;
                                                                                                                                                                                                                                                                                    41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Osteomodulin; fibromodulin; PRO216; human; angiogenesis;
                                        Mullen DG, Pierschbacher MD;
                                                                                                                                                                                                                                                                                  20; Mismatches
                                                                                                    Active fragments of protein esp. decorin
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY05767 standard; Protein; 421 AA.
                   (LJOL-) LA JOLLA CANCER RES FOUND.
                                                                                                                                            Claim 10; Page 41; 77pp; English.
92US-0865652
                                                                                                                                                                                                                                                                                                                                                                                                  |:| ||| ||| |||: |::|
122 KTLQELRAHENEITKVRK 139
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97US-0059117.
                                                                                                                                                                                                                                                                                                                                                                                    170 KSLAELRIHENKVKKIQK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0063329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                     Local Similarity 55.19 nes 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human osteomodulin PRO216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gerritsen ME,
                                        Craig W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC.
                                                                    WPI; 1993-336910/42.
                                                                                                                                                                                                                    as certain tumours
                                                                                                                                                                                                                                        139 AA;
                                                                                N-PSDB; AAQ50049
                                                   Ruoslahti EI;
03-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                        Cardenas J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9914234-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-SEP-1997;
                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY05767;
                                                                                                                        activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fong S,
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 41
AAY05767
ID AAY05
                                                                                                                                                                                                                                                                                 Matches
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207 IFAKMEKIMQLNICSNRLESMPPGLPSSLMYLSLENNSISSIPEKYFDKLPKLHTLRMSH 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 TNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKL--TKIHPKAFLTTKKLRRL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215 AFEGV-TVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGN 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274 NKITDIENGSLANIPRVREIHLENNKLKK---IPSGLPELKYLQIIFLHSNSIARVGVND 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immune related disease; diagnosis; antiinflammatory; cardiant; dermatological; antiarthritic; antirheumatic; immunosuppressive; haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anglogenic disorders (claimed), specifically cardiac hypertrophy (especially where associated with elevated levels of prostaglandin F2 alpha or induced by myocardial infarction), trauma (wounds, burns, or tissue regeneration more generally, including neurological disease), and cancer. Antagonists may be used similarly, also to treat age-related macular degeneration (or other anglogenic retinal disorders) and to prevent excessive growth of connective tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 DEDYDQEPDDDYQTGFPFRQNVDYGVPFHQYTLGCVSECFCPTNFPSSMYCDNRKLKTIP 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 DDDDDDDDDDDDDDDDDDDTFPTREPRSHFFPFDLFPM-CPFGCQC---YSRVVHCSDLGLTSVP 96
                                                                                                                                                                                                                                                                                                                                                                                        as human osteomodulin. The sequence is predicted from CDNA clone UN0190 or DNA33087-1158 (ATCC 209381, see AAX25419). Compositions containing PR0216, PR0230 (see AAV05764) and PR03102 (see AAV05768) is admixture with a carrier are claimed. The compositions are used to treat or prevent a wide range of cardiovascular, endothelial and
                                                                                                                                                                                                                                                                                                                                                              The present sequence represents human PRO216, which was identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                             Composition containing human polypeptides with anti-angiogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.4%; Score 366; DB 20; 29.3%; Pred. No. 1.8e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         during wound healing or in pulmonary fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human PRO216 protein UNQ190 SEQ ID NO:19.
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                                                                                                                                                                                                                                                                                      Example 1; Fig 6; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         320 MCPSIDPLHYHHLTYIRVDQNKLK 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JAN-2001 (first entry)
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Williams PM, Woodwi;
                                                                WPI; 1999-254381/21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 AA;
                                                                                                     N-PSDB; AAX25439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                      activity
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Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Henzel W;
systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune thrombocytopaenia; immune-mediated renal disease; demyelinating disease; hepatobiliary disease; Whipple's disease;
                                   inflammatory bowel disease; gluten-sensitive enteropathy; autoimmune disease; immune-mediated skin disease; allergic disease; immunological disease; transplantation associated disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gurney AL, Hebert C, He
D, Shelton DL, Smith V;
Wood WI, Yan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an J, Pennica D, Shelt
Watanabe CK, Wood WI,
                                                                  graft rejection; graft-versus-host-disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 33; Fig 8; 309pp; English.
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                                                                                                                                                                                                                                                                                                                              99US-0146222.
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Kabakoff RC, Lu Y, Pan
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                                                                                                                                                                                                                                                                                                                                                                                                           99US-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumas D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-572271/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAC58582
                                                                                                                WO200053758-A2.
                                                                                            Homo sapiens.
                                                                                                                                                           02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                    988;
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                                                                                                                                                                                                                                                                                                                                                                                                666
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                                                                                                                                      14-SEP-2000
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02-DEC-1
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treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, selected from systemic lupus erythematosus, rheumatoid arthritis, systemic selected from carthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogrem's systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases, allegic diseases, inflammatory bowel diseases including graft rejection and graft-versus-host-disease. AACS878 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AACS879 to AACS878 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                               nsed
for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267 NKLQDIPY-NIFNLPNIVELSVGHNKLKQAFYIPRNLEHL-----YLQNNEIEKMNLTV 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 -NIPMHIQOLYLQFNEIEAVTANSFINATHLKEINLSHNKIKSQKIDYGVFAKLPNLLQL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215 AFEGV-TVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGN 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 TNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKL--TKIHPKAFLTTKKLRRL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 DDDDDDDDDDDDDDDDDDTFPTREPRSHFFPFDLFPM-CPFGCQC---YSRVVHCSDLGLTSVP 96
proteins, anti-PRO antibodies, agonists and antagonists are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 DEDYDQEPDDDYQTGFPFRQNVDYGVPFHQYTLGCVSECFCPTNFPSSMYCDNRKLKTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 YLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 IFAKMEKLMOLNICSNRLESMPPGLPSSLMYLSLENNSISSIPEKYFDKLPKLHTLRMSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                              18.4%; Score 366; DB 21; Length 421; 29.3%; Pred. No. 1.8e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human PR0216 protein sequence SEQ ID NO:227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB24435 standard; Protein; 421 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       331 FCPTVPKMKKSLYSAISLFNNPVK 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          421 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200032221-A2.
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01-DEC-1998;

AAY88377 standard; Protein; 421 AA

RESULT 44

AAY8837

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angiogenic disorders in mammals (e.g. atherosolerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent nucleotide and protein sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                    Gerber H, Hillan KJ, Goddard A;
Kuo SS, Paoni NF, Smith V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention describes nucleic acids encoding PRO polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or anglogenic disorders in mammals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inappropriate PRO expression such as cardiovascular, endothelial or
                                                                                                                                                                                                                                                                                                      Ferrara N,
                                                                                                                                                                                                                                                                                                                  Klein RD,
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 72; Fig 96; 315pp; English.
                                                                                        99WO-US12252.
                                                                                                                                                99WO-US20111.
                                                                                                                                                                                              99WO-US21090.
                          99WO-US05028
                                                          99US-0131445
                                                                                                                  99US-0144758
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Williams PM,
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                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
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Watanabe CK,
                                                                                                    1999;
                                                                                                                  16661
                                                                                    02-JUN-1999;
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                                                                                                                                                                             13-SEP-1999;
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                                       12-MAR-1
28-APR-1
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                                                                                                                                                                                                                                                                   IFAKMEKLMQLNLCSNRLESMPPGLPSSLMYLSLENNSISSIPEKYFDKLPKLHTLRMSH 266
                                                                                                                                                                                                                                                                                                                                                                                                     274 NKITDIENGSLANIPRVREIHLENNKLKK---IPSGLPELKYLQIIFLHSNSIARVGVND 330
                                                                               DDDDDDDDDDDDDDDDTFPTREPRSHFFPFDLFPM-CPFGCQC---YSRVVHCSDLGLTSVP 96
                                                                                                        18.4%; Score 366; DB 21; Length 421; 29.3%; Pred. No. 1.8e-25; tive 73; Mismatches 138; Indels 18
                                         Conservative
                    Similarity
                                       95;
Query Match
                       Local
                                       fatches
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421 AA;

Sequence

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(vitellogenic carboxypeptidase homologue) polypeptide, or an agonist or antagonist of these. Also included in the invention is a method for preparing the composition, agonists and antagonists of PRO230, PRO216 or PRO302, and antibodies that bind to a PRO330, PRO316 or PRO302, polypeptides. The composition of the invention has cardiant, angiogenic, cytostatic, ophthalmic, and antiprolliferative activity. Analysis of the preval of expression of a gene encoding a PRO230, PRO216 or PRO302 polypeptide or detecting the presence/absence of the polypeptide is useful for diagnosis of cardiovascular, endothelial or angiogenic disorders in mammals. Anti-PRO230, PRO216 or PRO302 antibodies are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in these diagnostic methods. The PRO230, PRO216 or PRO302 polypeptides fond their coding sequences), agonists and antagonists are useful for treatment of cardiovascular, endothelial or angiogenic disorders, especially cardiac hypertrophy (especially characterized by presence of an elevated level of PGF-2alpha), trauma or cancer, myocardial infarction or age-related macular degeneration. In particular, PRO216, an agonist of PRO230, PRO216 or PRO20, an anti-PRO216 antibody is useful for inhibition of endothelial cell growth in a mammal. Endothelial cell growth can be stimulated by administration of PRO230, an anti-PRO300 agonist or an anti-PRO300 antibody and anti-PRO300 antibody. Additionally, an anti-PRO302 antibody can inhibit angiogenesis induced by PRO302 in a
                                                                                                                                Human, PR0216; Osteomodulin; fibromodulin; homologue; cardiant;
angiogenic; cytostatic; ophthalmic; antiproliferative activity;
cardiovascular; endothelial; angiogenic disorder; cardiac hypertrophy;
trauma; cancer; myocardial infarction; age-related macular degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the human PRO216 amino acid sequence. PRO216 is a human osteomodulin/fibromodulin homologue. The invention relates to a composition comprising a PRO230 (tubulointerstitial nephritis antigen homologue), PRO216 (osteomodulin/fibromodulin homologue) or PRO302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A composition comprising PRO230, PRO216 or PRO302 polypeptides, agonists or antagonists useful for promotion or inhibition of cardiovascularisation, angiogenesis or endothelialisation in mammals
                                                                                      PRO216 (osteomodulin/fibromodulin homologue) protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goddard A, Gurney AL, Hillan KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Fig 4; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0100262
                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-US19177.
                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                               WO200015792-A2
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                                              20-JUL-2000
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  AAY88377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secretory and transmembrane; PRO; mammalian; cancer; lung; brast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.
                                                                                                                                            TNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKL--TKIHPKAFLTTKKLRRL 154
                                                                                                                                                                                                                              215 AFEGV-TVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGN 273
                                                                                                                                                                                                                                            274 NKITDIENGSLANIPRVREIHLENNKLKK---IPSGLPELKYLQIIFLHSNSIARVGVND 330
                                                                                                                                                                             155 YLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPG 214
                                                  Gaps
                                                                          DDDDDDDDDDDDDDDDLFPTREPRSHFFPFDLFPM-CPFGCQC---YSRVVHCSDLGLTSVP 96
                                                                                                28 DEDYDGEPDDDYQTGFPFRQNVDYGVPFHQYTLGCVSECFCPTNFPSSMYCDNRKLKTIP 87
                                                                                                                                                                                                    147 HLEHNNLEEFPFPLPKSLERLLLGYNEISKLQTNAMDGLVNLTMLDLCYNYLHDSLLKDK
                                                  18;
                          Length 421;
                                                  73; Mismatches 138; Indels
                         18.4%; Score 366; DB 21; 29.3%; Pred. No. 1.8e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                       AAU12322 standard; Protein; 421 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human PRO216 polypeptide sequence.
                                                                                                                                                                                                                                                                                                                                 331 FCPTVPKMKKSLYSAISLFNNPVK 354
                                                                                                                                                                                                                                                                                                                                                         320 MCPSIDPLHYHHLTYIRVDONKLK 343
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2000WO-US04342.
2000WO-US04414.
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2000WO-US03565.
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2000WO-US05601.
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99WO-US28565
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                                                  Conservative
                                     Similarity
 421 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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16-DEC-1999;
20-DEC-1999;
20-DEC-1999;
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18-FEB-2000;
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06-JAN-2000;
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24-FEB-2000;
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  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU12322;
                         Query Match
                                        Local
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                                                   Matches
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tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or differentiation of chondrocytes, the proliferation or differentiation of chondrocytes, the proliferation of inner ear utricular supporting cells of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCS), or the proliferation of endothedial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adhocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU12172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectrical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of
                                                                                                                                                                                                                                                                                                                                                                                                                                           3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 HLEHNNLEEFPFFPFPKSLERLLLGYNEISKLQTNAMDGLVNLTMLDLCYNYLHDSLLKDK 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bloactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 DEDYDGEPDDDYQTGFPFRQNVDYGVPFHQYTLGCVSECFCPTNFPSSMYCDNRKLKTIP 87
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gao
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Deforge L, Desnoyers L, Filvaroff E, Ge
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Fig 302; 813pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lung, breast, prostate, cervical
                                                                   30 MAR-2000; 2000MO-US08439.
17-MAY-2000; 2000MO-US13705.
22-MAY-2000; 2000MO-US14042.
30-MAY-2000; 2000MO-US14941.
02-JUN-2000; 2000MO-US15264.
10-NOV-2000; 2000MO-US30873.
2000WO-US07377
                                                                                                                                                                                                                                                                                                                                                                                                         Laker KP, Beresini M, Del
Gerritsen ME, Goddard A,
Smith V, Stewart ma
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                                     21-MAR-2000;
30-MAR-2000;
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Composition comprising a PRO230, PRO216 or PRO302 polypeptide, agonist or antagonist for promoting or inhibiting angiogenesis and/or
                                                                                                                  cardiovascularisation; trauma; wound; cancer; atherosclerosis;
cardiac hypertrophy; macular degeneration; cardiant;
antianglogenic; antiarteriosclerotic; hypotensive; antirheumatic;
antiarthritic; antiinflammatory; vulnerary; antitumour; diagnosis;
                                                                                                                                                                                                                                                                                               "O-phosphorylated by casein kinase II"
                                                                                                                                                                                                                                                                                                    .251
.e= "O-phosphorylated by casein kinase II"
                                                                                                                                                                                                                                                                                                                    .275
.c= "O-phosphorylated by tyrosine kinase"
                                                                                                                                                                                                                                                                                                                                             "O-phosphorylated by tyrosine kinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goddard A, Gurney AL, Hillan KJ;
                                                                                                          PRO216; osteomodulin; fibromodulin; human; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                             "leucine zipper pattern"
                                                                                                                                                                                                                                                                                                                                                                                            /note= "leucine zipper pattern"
                                                                                                                                                                                                 "Asn is N-glycosylated"
                                                                                                                                                                                                                                               "Asn is N-glycosylated"
                                                                                                                                                                                                                                                               /note= "Asn is N-glycosylated"
[13..117
                                                                                                                                                                                                                 "Asn is N-glycosylated"
                                                                                                                                                                                                                                 "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                               "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                             "N-myristoylated"
                                                                                                                                                                                   Location/Qualifiers
                                             AAB20340 standard; Protein; 421 AA
320 MCPSIDPLHYHHLTYIRVDQNKLK 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cardiovascularisation in mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 55; Fig 4; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US28214
                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US20944.
                                                                             (first entry)
                                                                                                                                                                                                                                       .246
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300..307
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217..239
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                                                                                                                                                                                                                                                                                                                                              /note=
230..23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerritsen ME,
PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-235264/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAF30501.
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                                                                                            Human PRO216
                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                         29-NOV-1999;
                                                                            29-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAR-2001
                                                             AAB20340;
                                                                                                                                                    therapy.
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                                                                                                                                                                                                                                                                                                                                                                    Region
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                             RESULT 46
                                     AAB20340
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agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or anglogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration rheumatoid arthritis, angina, myocardial infarction, arterial restenosis, thrombophleabitis and lymphagitis. The polypeptides, agonists and antagonists are also used in claimed methods of stimulating or inhibiting endothelial cell growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 -NIPMHIQQLYLQFNEIEAVTANSFINATHLKEINLSHNKIKSQKIDYGVFAKLPNLLQL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 YLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 AFEGY-TVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGN 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NKITDIENGSLANIPRVREIHLENNKLKK---IPSGLPELKYLQIIFLHSNSIARVGVND 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; PRO; antiinflammatory; ophthalmological; vasotropic; retinal cell injury; ocular disease; retinitis pigmentosa; macular degeneration; retinal detachment; retinal tear; retinopathy; retinal degenerative disease; macular hole; degenerative myopia; acute retinal necrosis syndrome; traumatic chorioretinopathy; purtscher's retinopathy; oedema; ischaemic condition; retinal vision occlusion; collagen vascular disease; retinal vision purpura; uveitis; retinal vasculitis; Eales disease; systemic lupus erythematosus; environmental trauma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 DEDYDQEPDDDYQTGFPFRQNVDYGVPFHQYTLGCVSECFCPTNFPSSMYCDNRKLKTIP 87
The present sequence is that of human PRO216, a novel protein (49 kDa, pI 5.51) that is a homologue of osteomodulin and fibromodulin. The sequence is predicted from isolated PRO216 cDNA (see ART30501). PRO216 has a probable role in control of bone matrix deposition and/or osteoblast growth. PRO216 is 1 of 3 novel PRO polypeptides of the invention. PRO230, PRO216 and PRO302 polypucleotides and polypeptides, recombinant retroviral particles, ex vivo producer cells, expression vectors, host cells, and methods of recombinant production are provided, as well as antibodies, agonists and antagonists. The polynucleotides, polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 DDDDDDDDDDDDDDDDSLFPTREPRSHFFPFDLFPM-CPFGCQC---YSRVVHCSDLGLTSVP 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.4%; Score 366; DB 22; Length 4: 29.3%; Pred. No. 1.8e-25; ive 73; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU81955 standard; Protein; 421 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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Matches
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99WO-US28214.
99WO-US28313.
                                                      2000WO-US00219.
                                                          2000WO-US00376.
2000WO-US03565.
                                                                         2000WO-US04414.
                                                                                      2000WO-US06884.
                  2000WO-US20710
                                    99WO-US21090
                                                                    2000WO-US04341
                                                                             2000WO-US05004
                                                                                 2000WO-US05841
                                                  99WO-US28301
                                                                                           2000WO-US08439
                                                                                               2000WO-US13705
WO200109327-A2
                  28-JUL-2000;
                                                           06-JAN-2000;
11-FEB-2000;
                                                                    18-FEB-2000;
22-FEB-2000;
                                                       05-JAN-2000;
                                                                             24-FEB-2000;
                                                                                 02-MAR-2000;
                                                                                       15-MAR-2000;
                                                                                          30-MAR-2000;
17-MAY-2000;
                                    15-SEP-1999
                                         29-NOV-1999
                                              30-NOV-1999
                                                  01-DEC-1999
         08-FEB-2001
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# (GETH ) GENENTECH INC.

Gurney AL; Mark MR, Marsters SA, Pitti RM; Goddard A, Godowski PJ, Ashkenazi AJ, Baker KP, Kljavin IJ, Lafleur M, Wood WI; 2002-130120/17. Watanabe CK,

# N-PSDB; ABK28567

Promoting survival of retinal cells, or delaying or preventing retinal cell injury or death, by contacting retinal cells with PRO175, 220, 216, 243, 306, 346, 322, 536, 943, 840, 828, 826, 1068 or PRO1132 polypeptide -

# Claim 44; Fig 6; 152pp; English.

The invention relates to promoting the survival of retinal cells, or delaying or preventing retinal cell injury or death, by contacting the retinal cells with the polypeptide such as PRO17, PRO220, PRO316, PRO343, PRO343, PRO340, PRO320, PRO316, PRO343, PRO340, PRO3400, PRO3400 ischaemic condition, central or branch retinal vision occlusion, collagen vascular disease, thrombocytopaenic purpura, uveitis, retinal vasculitis, occlusion associated with Eales disease or systemic lupus erythematosus), retinal injury or environmental trauma. The retinal cell injury or death is delayed or prevented by substantially not causing angiogenesis or mitogenesis. The present sequence represents a PRO protein.

### 421 AA; Seguence

18.4%; Score 366; DB 23; Length 421; 29.3%; Pred. No. 1.8e-25; Live 73; Mismatches 138; Indels 18; Gaps Local Similarity 29.39 tes 95; Conservative Query Match Matches

8

The present invention relates to bone marrow expressed polynucleotides and proteins. These sequences can be used in the treatment of inflaumatory conditions (eg arthritis, Crohn's disease), cancer, central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's and Huntington's diseases, spinal cord disorders, head trauma, cerebrovascular diseases, myeloid and lymphoid cell disorders, platelet disorders, stem cell disorders, bone degenerative disorders, autoimmune disorders, for example multiple

Claim 10; Page 329-330; 380pp; English.

remodeling

41 DDDDDDDDDDDDDDDDDTFPTREPRSHFFPFDLFPM-CPFGCQC---YSRVVHCSDLGLTSVP 96 28 DEDYDOEPDDDYQTGFPFRQNVDYGVPFHQYTLGCVSECFCPTNFPSSMYCDNRKLKTIP 87 δŏ Pp

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Human: bone marrow; cytostatic; antirheumatic; antiarthritic; vulnerary; antinflammatory; antibacterial; immunosuppressive; vasotropic; cancer; antiparkinsonian; neuroprotective; noofropic; haemostatic; osteopathic; antiulcer; fungicide; antidiabetic; antiasthmatic; antiallergic; immunostimulant; analgestc; cerebroprotective; antianaemic; infection; nervous system disorder; autoimmune disorder; inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New bone marrow-expressed nucleic acids and polypeptides, useful for diagnosis, treatment of inflammatory, autoimmune, neurological, cancer and increasing hematopolesis, stem cell survival and bone growth and
                                                                                                                                                                                                                                    267 NKLQDIPY-NIFNLPNIVELSVGHNKLKQAFYIPRNLEHL-----YLQNNEIEKMNLTV 319
                               88 -NIPMHIQQLYLQFNEIEAVTANSFINATHLKEINLSHNKIKSQKIDYGVFAKLPNLLQL 146
                                                                                                147 HLEHNNLEEFPFPLPKSLERLLIGYNEISKLQTNAMDGLVNLTMLDLCYNYLHDSLLKDK 206
                                                                                                                                           215 AFEGV-TVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGN 273
                                                                                                                                                                          207 IFAKMEKLMQLNLCSNRLESMPPGLPSSLMYLSLENNSISSIPEKYFDKLPKLHTLRMSH 266
                                                                                                                                                                                                              274 NKITDIENGSLANIPRVREIHLENNKLKK---IPSGLPELKYLQIIFLHSNSIARVGVND 330
97 TNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKL--TKIHPKAFLTTKKLRRL 154
                                                                      155 YLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human bone marrow expressed protein SEQ ID NO: 277.
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                                                                                                                                                                                                                                                                                                                                                                                                             ABB12438 standard; Protein; 772 AA.
                                                                                                                                                                                                                                                                                    331 FCPTVPKMKKSLYSAISLFNNPVK 354
                                                                                                                                                                                                                                                                                                                        320 MCPSIDPLHYHHLTYIRVDQNKLK 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
23-AUG-2000; 2000US-0649267.
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzebaer's; Parkinson's disease; Humenostatic; amyotrophic lateral sclerosls; Shy-Drager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                                                                                                                                                                                                      379 DEDYDQEPDDDYQTGFPFRQNVDYGVPFHQYTLGCVSECFCPTNFPSSMYCDNRKLKTIP 438
                                                                                                                                                                                                                                                                                                  97 TNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKL--TKIHPKAFLTTKKLRRL 154
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                                                                                                                                                                                                                                                                                                                                                                                                                  215 AFEGV-TVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGN 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          439 -NIPMHIQOLYLQFNEIEAVTANSFINATHLKEINLSHNKIKSQKIDYGVFAKLPNLLQL 497
                                                                                                                                                                                Gaps
sclerosis, diabetes and arthritis, viral and bacterial infections, allergies and blood coagulation disorders. The present sequence is a
                                                                                                                                                                                                                  41 DDDDDDDDDDDDDDSLFPTREPRSHFFPFDLFPM-CPFGCQC---YSRVVHCSDLGLTSVP 96
                                                                                                                             18.4%; Score 366; DB 22; Length 772;
29.3%; Pred. No. 4.3e-25;
ive 73; Mismatches 138; Indels 18;
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Yang Y,
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Xu C, Xue AJ,
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2000US-0552317.
2000US-0598042.
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Wang Z, Wehrman T,
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2000US-0653450.
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2000US-0693036.
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                                                                                                                                                                       95; Conservative
                                              protein of the invention.
                                                                                                                                                   Best Local Similarity
                                                                                       772 AA;
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09-JUL-2000;
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03-AUG-2000;
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19-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        leukaemia.
                                                                                         Sequence
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                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang J,
                                                                                                                                                                         Matches
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7;
                                                                                                                                                                                                                                                                                                                                                                           the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate, cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 NALHVLEMSANPLDNNGIEPGAF-EGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKI 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 STVELEDFKRYKELQRLGLGNNKITD--IENGSLANIPRVREIHLENNKLKKIPSGLPEL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGM 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 STIPLHAFKGLNSLRRLVLDGNLLANQRIADDTFSRLQNLTELSLVRNSLAAPPLNLPS- 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                 The invention relates to human nucleic acids (AAI57798-AAI61369) and
                                                                                                                                                                            useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 CPSVCRCDNGFIYCNDRGLTSIPADIPDDATTLXLQNNQI------N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.2%; Score 363.5; DB 22; Length 32.7%; Pred. No. 6e-25; ive 51; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 KYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNN 351
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Zhao QA, Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                             such as central nervous system injuries
                                                                                                                                                                        Novel nucleic acids and polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human PRO1483 polypeptide sequence.
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Best Local Similarity 32.78
Matches 92; Conservative
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                                                              2001-442253/47.
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                                                                                                   N-PSDB; AAI59382
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33; Gaps

51; Mismatches 105; Indels

92; Conservative

Matches

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the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VITA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chodrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU12172-AAU12446 represent novel human secretory and transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deforge L, Desnoyers L, Filvaroff E, Ga
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; Fig 36; 813pp; English.
                                                                                                                                                                                                                                          2000WO-US00376.
2000WO-US03565.
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2000WO-US07532.
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2000WO-US14941.
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99WO-US28565
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Smith V, Stewart TA,
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30-DEC-1999;
06-JAN-2000;
06-JAN-2000;
11-FEB-2000;
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18-FEB-2000;
22-FEB-2000;
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20-MAR-2000;
21-MAR-2000;
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02-DEC-1999;
09-DEC-1999;
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24-FEB-2000;
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30-MAY-2000;
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07-JUN-2001
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Gao W;

Score 363.5; DB 22; Length 674; Pred. No. 6e-25;

18.28;

Query Match Best Local Similarity

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74 CPFGCQCYSRVVHCSDLGLISVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
                                                                                                                                              253 STVELEDFKRYKELQRLGLGNNKITD--IENGSLANIPRVREIHLENNKLKKIPSGLPEL 310
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                                                                                                             134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGM 193
                                                                                                                                                                                                                           194 NALHVLEMSANPLDNNGIEPGAF-EGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKI
                                                                                                                                                                                                                                                        311 KYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNN 351
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                                                        54 CPSVCRCDNGFIYCNDRGLTSIPADIPDDATTLYLQNNQI---
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Copyright (c) 1993 - 2003 Compugen Ltd.
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protein - protein search, using sw model ĕ January 24, 2003, 12:24:30 ; Search time 17 Seconds Run on:

(without alignments) 655.958 Million cell updates/sec

US-09-944-457-2

Perfect score:

1 MKEYVLLLFLALCSAKPFFS.........PATFRCVLSRMSVQLGNFGM 379 Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

262574 seqs, 29422922 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 50 summaries

Database :

Issued\_Patents\_AA:\*

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/cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
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/cgn2\_6/ptodata/1/iaa/PcTUS\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/PcTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMADIES

	Description	Sequence 43, Appl	· ~	. ~	Patent No. 5340934	. 4	Sequence 4, Appli	7	ì	Sequence 2, Appli	Sequence 27. Appl	Patent No. 5340934	Sequence 48, Appl	Sequence 45, Appl	Sequence 42. Appl	Sequence 39. April	Sequence 36. Appl	Sequence 2. Appli	i	ì		ζ.	Sequence 305. App	-	ì -	, ,		7
SUMMARIES	ID	US-09-724-864-43	US-08-303-238-3	US-08-458-834-3	34-2	US-08-303-238-4	US-08-458-834-4	US-08-272-919-2	US-08-619-916-2	PCT-US95-08542-2	US-08-442-063A-27	5340934-4	US-08-442-063A-48	US-08-442-063A-45	US-08-442-063A-42	US-08-442-063A-39	US-08-442-063A-36	US-08-303-238-2	US-08-458-834-2		~	US-09-540-153-2	US-09-188-930-305	US-08-303-238-1	US-08-458-834-1	-191-	245	US-09-540-153-7
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28	316	15.9	1480	2	391-09055	Sequence 2, Appli
29	313	15.7	1480	4	US-09-182-024A-5	'n
30	309	15.5	1523	4	US-09-182-024A-2	7
31	296	14.9	1091	m	US-08-986-485-5	, L
32	272	13.7	603	-	US-08-190-802A-50	50,
33	272	13.7	603	4	US-08-477-346-50	50,
34	272	13.7	603	4	US-08-473-089-50	50,
35	272	13.7	603	4	4 US-08-487-072A-50	Sequence 50, Appl
36	262	13.2	708	4	US-09-131-648-2	2.7
37	259.5	13.0	1101	٣	US-08-986-485-2	7
38	256.5	12.9	96	Н	US-08-442-063A-33	33
39	254	12.8	353	æ	US-08-986-485-6	9
40	246	12.3	605	Н	US-08-190-802A-49	49
41	246	12.3	605	4	US-08-477-346-49	49
42	246	12.3	605	4	US-08-473-089-49	49
43	246	12.3	605	4	US-08-487-072A-49	49
44	241	12.1	605	4	us-09-063-950-5	'n
45	241	12.1	673	4	US-09-063-950-2	7
46	239	12.0	180	3	US-08-986-485-8	· &
47	236	11.8	440	m	US-08-985-335-3	'n
48	236	11.8	440	4	US-09-410-372-3	'n
49	222	11.1	224	Ŋ	PCT-US91-09055-4	4
20	212.5	10.7	298	4	US-09-232-160-17	Sequence 17, Appl
					ALIGNMENTS	
RESULT	1					
LS-09-7	US-09-724-864-43	~				
Segme	Segmence 43. Application HS/09724864	Applicat	SII doi:	.60/	724864	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 FKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHEN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 TLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Watson, James D
APPLICANT: Watson, James D
APPLICANT: Watson, James G.
TITLE OF INVENTION: Polynucleotides, polypeptides expressed
TITLE OF INVENTION: by the polynucleotides and methods for their use.
TITLE REFRENCE: 11000.105011
CURRENT APPLICATION NUMBER: US/09/724,864
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
PRIOR FILING DATE: 1999-112-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.3%; Score 1799; DB 4; Length 373; 90.2%; Pred. No. 3.9e-170; Live 17; Mismatches 14; Indels
Sequence 43, Application US/09724864 Patent No. 6380362 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Mouse
US-09-724-864-43
                                                                                                                                                                                                                                                                        SEQ ID NO 43
LENGTH: 373
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301 KKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQP 360
                     295 KKIPSGLQELKYLQIIFLHYNSIAKYGVNDFCPTVPKMKKSLYSAISLFNNPMKYWEIQP 354
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                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BORDER, WAYNE A.

TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS

TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING
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REFERENCE/DOCKET NUMBER: P-LA 9453
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: PIERSCHBACHER, MICHAEL D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/978,931
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                           Sequence 3, Application US/08303238 Patent No. 5654270
                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: LONGAKER, MICHAEL T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                     WHITBY, DAVID J. HARPER, JOHN R.
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                                                                                                          361 ATFRCVLSRMSVQLGNFG 378
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619-535-8949
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amino acid
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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APPLICANT:
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US-08-303-238-3
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291 RVPSGLPDLKLLQVVYLHSNNITKVGVNDFCPMGFGVKRAYYNGISLFNNPVPYWEVQPA 350
182 VKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPT 241
                                                                                                                                                                302 KIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPA 361
                                                                               242 LLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLK 301
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Best Local Similarity 52.4%; Pred. No. 5e-93;
Matches 197; Conservative 64; Mismatches 95; Indels 2
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APPLICATION NUMBER: US/08/458,834
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4370 LA JOLLA VILLAGE DRIVE, SUITE 700
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APPLICANT: PIERSCHBACHER, MICHAEL D.
APPLICANT: BORDER, WAYNE A.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,931
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LONGAKER, MICHAEL T.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 34,202
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619-535-8949
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                                                                                                                                                                                                                                                    362 TFRCVLSRMSVQLGNF 377
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MOLECULE TYPE: protein
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                                                                                                                                                122 KGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENK
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; Patent No. 5340934
; ROBEY, PAMELA G.
; ROBEY, PAMELA G.
; TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.2%; Score 1020; DB 6; Length 368; 52.1%; Pred. No. 6.3e-93; tive 66; Mismatches 94; Indels 2
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APPLICATION NUMBER: US/07/432,044
FILING DATE: 03-NOV-1989
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Best Local Similarity 52.1%
Matches 196; Conservative
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5340934-2
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239 PPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENN 298
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                                                                                                                                                                                                     APPLICANT: BORDER, WAYNE A.
TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 -----FEPSLGPVCPFRCQCHLRVVQCSDLGLDKVPRDLPPDTTLLDLQNNKITEIKDG 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,238
                                                                                                                                                                                                                                                                                                         E: CAMPBELL AND FLORES
4370 LA JOLLA VILLAGE DRIVE, SUITE 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: P-LA 9453
TELECOMMUNICATION INFORMATION:
                                                                                                                                        WHITBY, DAVID J.
HARPER, JOHN R.
PIERSCHBACHER, MICHAEL D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,931
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
                                    Sequence 4, Application US/08303238 Patent No. 5654270
                                                                                                 RUOSLAHTI, ERKKI I.
LONGAKER, MICHAEL T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: KONSKI, ANTOINETTE F. REGISTRATION NUMBER: 34,202
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Matches 191; Conservative (
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619-535-8949
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CLASSIFICATION: 514
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                                                                         GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
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                 US-08-303-238-4
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Best Local 8
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RESULT 5
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351 TFRCVTDRLAIQFGNY 366

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SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0, V (2, 08/08/272,919 08-JUL-1994 N: 435
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Craig, William S. APPLICANT: Harper, John R. APPLICANT: Hernandez, Sam D. APPLICANT: Kostel, Paul J. APPLICANT: Parker, Jonathan R. APPLICANT: Vedvick, Thomas S. APPLICANT: Vedvick, Thomas S.
                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08272919
Patent No. 5567807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                          359 QPATFRCVLSRMSVQLGNF 377
                                                                                                                                                                                                                                                    340 QPSTFRCVYVRSAIQLGNY 358
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LENGTH: 342 amino acids
TYPE: amino acid
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Best Local Similarity 53.99
Matches 178; Conservative
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; MOLECULE TYPE: protein
US-08-272-919-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 NKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGL 238
280 KLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFSNPVQYWEI 339
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                                                                                                                                                                                                                                                                                                                                                 APPLICANT: PIERSCHBACHER, MICHAEL D.
APPLICANT: BORDER, WAYNE A.
TITLE OF INVENTO: INHIBITORS OF CELL REGULATORY FACTORS
TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKEYVLLLFLALCS-AKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDSDVSLFPTR 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: CAMPBELL AND FLORES 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,931
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/458,83
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 34,202
REFRENCE/POCKET NUMBER: P-LA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
                                                                                                                                                                                                     Sequence 4, Application US/08458834
Patent No. 6277812
                                                                                                                                                                                                                                                                     RUOSLAHTI, ERKKI I.
LONGAKER, MICHAEL T.
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HARPER, JOHN R.
                                                               359 QPATFRCVLSRMSVQLGNF 377
                                                                                                   340 OPSTFRCVYVRSAIOLGNY 358
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CORRESPONDENCE ADDRESS:
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APPLICANT:
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TITLE OF INVENTION: Processes for the Purification of Human IIILE OF INVENTION: Recombinant Decorin and the Detection of Guanidinium Ions
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PPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENN 298
                                                                                                                                                         220 PPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHLRELHLDNN 279
                                                                                                                                                                                                                            299 KLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEM 358
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Recombinant Decorin and the Detection of Guanidinium
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109 QNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNL 168
                         228 EAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANI 287
                                                                                                                                                                                                                                                288 PRVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAIS 347
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                                                                                 169 PKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application PC/TUS9508542
GENERAL INFORMATION:
APPLICANT: La Jolla Cancer Research Foundation
                                                                                                                                                                                                                                                                                                                                                       313 LFSNPVQYWEIQPSTFRCVYVRSAIQLGNY 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US95/08542
FILING DATE: 07-JUL-1995
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NAME: Perkins, Susan M.
REGISTRATION NUMBER: 36,405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-849
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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Matches 178; Conservative
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TITLE OF INVENTION: Huma
TITLE OF INVENTION: Rec
TITLE OF INVENTION: LONG
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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STATE: California
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APPLICANT: Craig, William S.
APPLICANT: Harper, John R.
APPLICANT: Hernandez, Sam D.
APPLICANT: Parker, Jonathan R.
APPLICANT: Parker, Jonathan R.
APPLICANT: Parker, Jonathan R.
APPLICANT: Parker, Jonathan R.
APPLICANT: Percesses for the Purification of Human
TITLE OF INVENTION: Recombinant Decorin and the Detection of Guanidinium Ions
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                                                                                                                                                                                        253 PHLRELHLDNNKLTRVPGGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVS 312
                           288 PRVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAIS 347
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  PKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIA 227
                                                                                   EAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANI 287
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APPLICATION NUMBER: US 08/272,919
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/619,916
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Patent No. 5763276
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IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
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CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 435
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STATE: California
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                                                                                                                     EAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANI 287
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APPLICANT: RUGSLAHIT, ERKKI I.

APPLICANT: PIERSCHABCHER, MICHAEL D.

APPLICANT: CARDENAS, JOSE
APPLICANT: CRAIG, WILLIAM
APPLICANT: MULLIAM
AP
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4370 LA JOLLA VILLAGE DRIVE, SUITE 700
                                                                                                                                                                                                                                                                                                                                                                                                 348 LFNNPVKYWEMQPATFRCVLSRMSVQLGNF 377
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APPLICATION NUMBER: US/08/442,063A
FILING DATE: 16-MAY-1995
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REFERENCE/POCKET NUMBER: P-LA 1454
TELECOMMUNICATION INFORMATION:
TELECHONE: 619-535-9001
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APPLICATION NUMBER: US 07/865,652
FILING DATE: 03-APR-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         333 amino acids
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: UNITED STATES
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
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110 NNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLP 169
                                                   62 NNKITEIKDGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMP 121
                                                                                                                                       229 AKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIP 288
                                                                                                                                                                                                                                                 289 RVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISL 348
                                                                                                                                                                                                                                                                                                                                                              126 SLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 GGLAEHKYIQVVYLHNNNISVVGSSDFCPPGHNTKKASYSGVSLFSNPVQYWEIQPSTFR 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 FPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 QKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGLPPTLLE 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIP 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 FEPSLGPVCPFRCQCHLRVVQCSDLGLDKVPRDLPPDTTLLDLQNNKITEIKDGDFKNLK 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 LLLFLALCSAKPFFSPSHIALKNWMLKDMEDTDDDDDDDDDDDDDDDDDDDDDDDFFFFF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LILLIAQVSWAGPF---QQRGLFDFMLEDEASGIGPEVPDDRD------39
                                                                                                       170 KSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROBEY, PAMELA G. TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: TERMINE, JOHN D.; YOUNG, MARIAN F.; FISHER, LARRY W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.5%; Score 907; DB 6; 49.1%; Pred. No. 9.4e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      349 FNNPVKYWEMQPATFRCVLSRMSVQLGNF 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/432,044
FILING DATE: 03-NOV-1989
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Matches 183; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Patent No. 5340934
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US-08-442-063A-48
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50 DEDNSLFPTREPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQ 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289 RVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISL 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 42.5%; Score 847; DB 1; Length 307; Best Local Similarity 53.3%; Pred. No. 6.7e-76; Matches 162; Conservative 56; Mismatches 84; Indels
                                                                                                     TITLE OF INVENTION: DECORIN FRACMENTS AND METHODS OF TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS NUMBER OF SEQUENCES: 62
                                                                                                                                                                                         3: CAMPBELL AND FLORES 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,652
FILING DATE: 03-APR-1992
ATORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/POCKET NUMBER: P-LA 1454
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEPHONE: 619-535-9001
RUOSLAHTI, ERKKI I.
PIERSCHBACHER, MICHAEL D.
CARDENAS, JOSE
CRAIG, WILLIAM
MULLEN, DANIEL G.
                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,063A
FILLIO DATE: 16-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                       COUNTRY: UNITED STATES ZIP: 92122
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MOLECULE TYPE: protein
US-08-442-063A-48
                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                              CITY: SAN DIEGO
STATE: CALIFORNIA
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Best Local Similarity
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                                                                                 APPLICANT:
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                     APPLICANT
                                           APPLICANT
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US-08-442-063A-45

RESULT 13

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50 DEDNSLFPTREPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQ 109
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APPLICANT: PIERSCHBACHER, MICHAEL D.
APPLICANT: CARDENAS, JOSE
APPLICANT: CRAIG, WILLIAM
APPLICANT: RULER, DANIEL G.
TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS OF
TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.0%; Score 776; DB 1; Length 282; 53.4%; Pred. No. 6.5e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

FILLING DATE: 16-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289 RVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIARVG 327
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,652
FILING DATE: 03-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PC-DOS/MS-DOS
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Sequence 45, Application US/08442063A Patent No. 5705609
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: CAMPBELL, CATHRYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1
TELECOMMUNICATION INFORMATION-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
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STATE: CALLFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
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                        Patent No. 5705609
GENERAL INFORMATION:
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PC-DOS/MS-DOS
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APPLICANT: CRAIG, WILLIAM
APPLICANT: MULLEN, DANIEL G.
ITLE OF INVENTION: DECORIN FR
TITLE OF INVENTION: INHIBITING
NUMBER OF SEQUENCES: 62
                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                 APPLICANT: MULLEN, DANIEL G. TITLE OF INVENTION: DECORIN ITITLE OF INVENTION: INHIBITIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 amino acids
  APPLICANT: CRAIG, WILLIAM
                                                                                                                                                                                                           UNITED STATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-442-063A-39
                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                          CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                  CITY: SAN DIEGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 TNITS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 AKLTS 233
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                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                              STREET:
                                                                                                                                                                                   STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 NNKITEIKDGDFKNLKNLHALILVNNKISKVSPGAFTPLVKLERLYLSKNQLKELPEKMP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 KSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAE 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.9%; Score 616; DB 1; Length 236; 52.4%; Pred. No. 3.6e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69; Indels
                                  APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: PIERSCHBACHER, MICHAEL D.
APPLICANT: CARDENAS, JOSE
APPLICANT: CARDENAS, JOSE
APPLICANT: CRAIG, WILLIAM
APPLICANT: MULLEN, DANIEL G.
TITLE OF INVENTION: DECORIN FRACMENTS AND METHODS OF
TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,063A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                            E: CAMPBELL AND FLORES
4370 LA JOLLA VILLAGE DRIVE, SUITE 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 39, Application US/08442063A
Patent No. 5705609
GENERAL INFORMATION:
APPLICANT: RUGSLAHTI, ERKKI I.
APPLICANT: PIERSCHBACHER, MICHAEL D.
APPLICANT: CARDENAS, JOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: P-LA 1454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,652
FILING DATE: 03-ARR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: CAMPBELL, CATHRYN A. REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 236 amino acids
                                                                                                                                                                                                                                                                                                               UNITED STATES
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                                                                                                                                                                                                                                                                                         CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                  STATE: CATTE
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                     GENERAL INFORMATION:
Patent No. 5705609
                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                            COUNTRY: UI
                                                                                                                                                                                                                            ADDRESSEE:
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50 DEDNSLFPTREPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQ 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 24.7%; Score 493; DB 1; Length 188; Best Local Similarity 53.0%; Pred. No. 4e-41; Matches 98; Conservative 32; Mismatches 53; Indels
TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS OF TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS NUMBER OF SEQUENCES: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DECORIN FRAGMENTS AND METHODS OF INHIBITING CELL REGULATORY FACTORS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,063A
FILING DATE: IC-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                    E: CAMPBELL AND FLORES
4370 LA JOLLA VILLAGE DRIVE, SUITE 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: CAMPBELL, CATHRYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1454
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 36, Application US/08442063A
Patent No. 5705609
GENERAL INFORMATION:
APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: PIERSCHBACHER, MICHAEL D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,652
FILING DATE: 03-APR-1992
ATTORNEY/AGENT INFORMATION:
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64 YGSPPQPEPRD-------CPQECDCPPNFPTAMYCDNRNLKYLPF-VPSRMKYVYFQ 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             287 NTFNSSSLLELDLSYNQLQKIP---PVSTNLENLYLQGNRINEFSISSFCTVVDVMNFSK 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 ----PTREPRSHFFPFDLFPMCPFGCQC---YSRVVHCSDLGLTSVPTNIPFDTRMLDLQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 NNKIKEIKENDFKGLTSLYGLILNNNKLT--KIHPKAFLTTKKLRRLYLSHNQLSEIPLN 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRI 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 AEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLA- 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 ---NIPRVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: RUGSLAHTI, ERKKI I.
APPLICANT: LONGAKER, MICHAEL T.
APPLICANT: WHITEY, DAVID J.
APPLICANT: HARPER, JOHN R.
APPLICANT: PIERSCHBACHER, MICHAEL D.
APPLICANT: PIERSCHBACHER, MICHAEL D.
APPLICANT: BORDER, WAYNE A.
TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 LLLFLALCSAK--PFFSPSHIALKNWMLKDMEDTDDDDDD-----DDDDDDDEDNSLF- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.2%; Score 342.5; DB 1; Length 3 27.7%; Pred. No. 9.2e-26; Live 66; Mismatches 158; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                      P-LA 9453
                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,238
                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,931
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                    NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/POCKET NUMBER: P-LA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 18
US-08-458-834-2
; Sequence 2, Application US/08458834
; Patent No. 6277812
                                                                                                                                                                                                                                                                                                                                                                    TELEBAX: 619-000 NO: 2 SEQUENCE CHARACTERISTICS: TENGTH: 375 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-303-238-2
                                                                                                                                      FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        343 YSAISLFNNPVK 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 NNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLP 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: RUGSLAHTI, ERKKI I.
APPLICANT: RUGSLAHTI, ERKKI I.
APPLICANT: LONGAKER, MICHAEL T.
APPLICANT: HERER, JOHN J.
APPLICANT: PIERSCHBACHER, MICHAEL D.
APPLICANT: BORDER, WAYNE A.
TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.3%; Score 384.5; DB 1; Length 141; 55.1%; Pred. No. 1.5e-30; tive 20; Mismatches 41; Indels 1
                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,063A
FILING DATE: 16-MAY-1995
CLASSIFFCATION: 514
                    E: CAMPBELL AND FLORES
4370 LA JOLLA VILLAGE DRIVE, SUITE 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
                                                                                                                                                                                                                                                                                                    FILING DATE: 16-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,652
FILING DATE: 03-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN A.
REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-LA 1454
                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAMPBELL AND FLORES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-303-238-2
; Sequence 2, Application US/08303238
; Patent No. 5654270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 KSLAELRIHENKVKKIOK 187
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122 KTLQELRAHENEITKVRK 139
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                                                                                  STATE: CALIFORNIA COUNTRY: UNITED STATES
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Matches 76; Conservative
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STATE: CALLFORNIA
COUNTRY: UNITED STATES
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CORRESPONDENCE ADDRESS:
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                                                               SAN DIEGO
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13;

Gaps

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PRIOR APPLICATION NUMBER: 60/081,057 PRIOR FILING DATE: 1998-04-07
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                                                                                                                                                                                                                                                 SOFTWARE: Patentin Ver. 2.0
                     APPLICANT: Brose, Katja
APPLICANT: Kid, Thomas
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ORGANISM: human
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SEQ ID NO 2
LENGTH: 1525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 ----PTREPRSHFFFFDLFPMCPFGCQC---YSRVVHCSDLGLTSVPTNIPFDTRMLDLQ 109
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                   ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFRENCE/DOCKET WUMBER: P-LA 9453
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,931
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,834
                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 27.7%
Matches 103; Conservative
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; MOLECULE TYPE: protein
US-08-458-834-2
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APPLICANT: Goodman, Corey
                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
  CORRESPONDENCE ADDRESS:
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APPLICANT: Kid, Thomas
APPLICANT: Kid, Thomas
APPLICANT: Tosse, Katja
APPLICANT: Tessier-Lavigne, Marc
APPLICANT: Tessier-Lavigne, Marc
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,245A
PRIOR APPLICATION NUMBER: 60/065,544
PRIOR FILING DATE: 1997-11.14
APPLICANT: Tessier-Lavigne, Marc TITLE OF INVENTYOR: Modulating Robo: Ligand Interactions FILE REFERENCE: B98-031-3 CURRENT APPLICATION NUMBER: US/09/191,647 CURRENT FILING DATE: 1998-11-13 EARLIER APPLICATION NUMBER: 60/065,544 EARLIER FILING DATE: 1997-11-14 EARLIER APPLICATION NUMBER: 60/065,546 EARLIER FILING DATE: 1998-04-07 NUMBER: 00.05: 14
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                                                           16.9%; Score 336; DB 4; Length 1525; 26.5%; Pred. No. 3.2e-24; ive 61; Mismatches 120; Indels 110
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APPLICANT: Except Katja
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REPERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,153
CURRENT APPLICATION NUMBER: 09/191,647
PRIOR APPLICATION NUMBER: 09/191,647
PRIOR PELICATION NUMBER: 60/081,057
PRIOR FILING DATE: 1998-04-07
NUMBER OF SEO ID NOS: 14
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Kid, Thomas
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Matches 105; Conserv
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ORGANISM: human
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LENGTH: 1525
                     US-09-540-245A-2
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283 SLANIPRVREIHLENNKLK----KIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKM 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 PTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGS--LANIPRVREIHLEN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---LDNNGIE 212
                                                                                                                                 456 TSGARCTSPRRLANKRIGQIKSKKFRCSGTEDYRSKLSGDCFADLACPEKCRCEGTTV-- 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----KVQRIYLYHNSLDEFPTNLPKYVKELHLQEN 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 KVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIR-IAEAKLTSVPKGLP 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 FQVAPLSVVAKSCPSVCRCDAGFIYCNDRSLTSIPVGIPEDATTLYLQNNQINNVGIPSD 78
                                                                                                                                                                                                    224 IRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELED-FKRYKELQRLGLGNNKITDIENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 649;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Streachan, Lorna APPLICANT: Streachan, Matthew APPLICANT: Sleeman, Matthew APPLICANT: Onrust, Rene APPLICANT: Onrust, Rene APPLICANT: MISSON, James Greg TITLE OF INVENTION: Compositions Isolated From Skin Cells TITLE OF INVENTION: and Methods For Their Use TILE CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09 CURRENT FILING DATE: 1998-11-09 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.8%; Score 334.5; DB 4; 31.8%; Pred. No. 1.3e-24; tive 40; Mismatches 112;
169 PKSLAELR---IHENKVKKIQKDTFKGMNALHVLEMSANP
                                                                                                                                                                                                                                                                                                                                                                                    624 GLSSVRLLSLYDNQIT--TVAAPGAFDTLHSLSTLNL 657
                                                                                                                                                                                                                                                                                                                                                      339 KKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSVQL 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 305, Application US/09188930A; Patent No. 6150502
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APPLICANT: Watson, James D.
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ORGANISM: Mouse
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US-09-188-930-305
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; Sequence 1, Application US/08303238

RESULT 23 US-08-303-238-1

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Local Similarity
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                     US-08-458-834-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 LGLGNNKITDIENGSLA----NIPRVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIA 324
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TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48; Gaps
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                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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4370 LA JOLLA VILLAGE DRIVE, SUITE 700
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                 APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: LONGAKER, MICHAEL T.
APPLICANT: WHITBY, DAVID J.
APPLICANT: HARPER, JOHN R.
APPLICANT: PIERSCHBACHER, MICHAEL D.
APPLICANT: BORDER, WAYNE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: P-LA 9453
TELECOMMUNICATION:
TELEPHONE: 619-535-9001
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,931
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/303,238
                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: KONSKI, ANTOINETTE F. REGISTRATION NUMBER: 34,202
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                                                                                                                                                                                                                                                              STATE: CALIFORNIA COUNTRY: UNITED STATES
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MOLECULE TYPE: protein
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                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                               CITY: SAN DIEGO STATE: CATTLE
GENERAL INFORMATION:
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Best Local Similarity
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92 LISVPINIPFDIRMLDLQNNKIKEIKENDFKGLISLYGLILNNNKLI--KIHPKAFLTIK 149
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                                                                                                                                                                                                                                                TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DAIA:
                                                                                                                                                                                                                                                                                                                                                                                        4370 LA JOLLA VILLAGE DRIVE, SUITE 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: P-LA 9453
TELECOMMUNICATION INFORMATION:
                                                                                                                                  APPLICANT: WHITBY, DAVID J.
APPLICANT: HARPER, JOHN R.
APPLICANT: PIERSCHBACHER, MICHAEL D.
APPLICANT: BORDER, WAYNE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/978,931 FILING DATE: 17-NOV-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/458,834
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Sequence 1, Application US/08458834 Patent No. 6277812
                                              GENERAL INFORMATION:
APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: LONGAKER, MICHAEL T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
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619-535-8949
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STATE: CALLFORNIA
COUNTRY: UNITED STATES
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                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                             APPLICANT: Erose, Katja
APPLICANT: Erose, Katja
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT ELING DATE: 1998-11-13
EARLIER PILING DATE: 1997-11-14
EARLIER PILING DATE: 1997-11-14
EARLIER FILING DATE: 1998-04-07
SOFTWARE: PATCH NOWBER: 60/081,057
EARLIER FILING DATE: 1998-04-07
SOFTWARE: PATCH NOWS: 14
SOFTWARE: PATCH NOW: 10
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APPLICANT: Kid, Thomas
APPLICANT: Brose, Katja
APPLICANT: Brose, Katja
APPLICANT: Pessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 KSLAELRI - - - HENKVKKIQKDTFKGMNALHVLEMSANPL - -
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                        327 EFSISSFCTVVDVVNFSKLQVVRLDGNEIK 356
325 RVGVNDFCPTVPKMKKSLYSAISLFNNPVK 354
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                                                                                                                      Sequence 7, Application US/09191647 Patent No. 6046015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98; Conservative
                                                                                                                                                                                  APPLICANT: Goodman, Corey
APPLICANT: Kid, Thomas
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                                                                                                                                                               GENERAL INFORMATION:
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US-09-540-245A-7
                                                                                          RESULT 25
US-09-191-647-7
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73 CPRVCSCTGLNVDCSHRGLTSVPRKISADVERLELQGNNLTVIYETDFQRLTKLRMLQLT 132
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APPLICANT: Goodman, Corey
APPLICANT: Kid, Thomas
APPLICANT: Kid, Thomas
APPLICANT: Brose, Katja
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
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       CURRENT PELLICATION NUMBER: US/09/540,245A
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/065,544
PRIOR FILING DATE: 1997-11-14
PRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 20
SEQ ID NO 7
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CURRENT APPLICATION NUMBER: US/09/540,153
CURRENT FILING DATE: 2000-03-31
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PRIOR PELICATION NUMBER: 60/081,057
NUMBER OF TELLING DATE: 1998-04-07
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BER: 09/191,647
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; ORGANISM: Drosophila melanogaster
US-09-540-153-7
                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-540-245A-7
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; Patent No. 6270995
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FILE REFERENCE: B98-031-3
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PRIOR FILING DATE: 1998-1
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Best Local Similarity
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APPLICANT: Connolly, Timothy
APPLICANT: Rajput, Bhanu
TITLE OF INVENTION: Human Slit Polypeptide and Polynucleotides Encoding
TITLE OF INVENTION: Same
TITLE OF INVENTION: Same
CURRENT APPLICATION NUMBER: US/09/182,024A
CURRENT FILING DATE: 1998-10-29
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                                                                                                                                                                                                                                                                                                                                                       COCATION METHOD: Array of Flank-LRR-Flank OTHER INFORMATION: mediates adhesive events OTHER INFORMATION: mediates adhesive events OTHER INFORMATION: mediates adhesive events LOCATION: 911 to 1150 IDBNTIFICATION METHOD: similarity to tandem EGF-like OTHER INFORMATION: protein-protein interactions NAME/KEY: 7th EGF-like repeat LOCATION: 1153 to 1393 IDBNTIFICATION METHOD: similarity to epidermal growth OTHER INFORMATION: Involvement in receptor-ligand LOCATION: 1394 to 1404 IDBNTIFICATION METHOD: experimental COCATION: 1394 to 1404 IDBNTIFICATION METHOD: experimental MANE/REY: Alternative splice segment MANE/REY: Alternative splice segment MANE/REY: Alternative splice segment MANE/REY: Alternative splice segment MANE/REY: Alternative method: experimental MANE/REY: Alternative method: experi
                                                                                                                                                                                                           IDENTIFICATION METHOD: similarity to other signal
                                                                                                                                                                                                                                         OTHER INFORMATION: Directs Export NAME/KEY: Four Flank-LRR-Flank domains
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LOCATION: 1405 to 1480
IDENTIFICATION METHOD: experimental
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                                                                                                                          signal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 25.18 nes 98; Conservative
                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                         37 to 910
TOPOLOGY: Linear
                                                                                                                          NAME/KEY:
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                                                                                                                                                            LOCATION:
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Sequence 2, Application US/09182024A

Sequence 2, Application US/09182024A

Patent No. 6342370

GENERAL INFORMATION:
APPLICANT: Connolly, Timothy
APPLICANT: Rajbut, Bhanu
TITLE OF INVENTION: Human Slit Polypeptide and Polynucleotides Encoding
TITLE OF INVENTION: Same
FILE REFERENCE: 640100-271

CURRENT APPLICATION NUMBER: US/09/182,024A

PRIOR FILING DATE: 1997-10-31

PRIOR APPLICATION NUMBER: 60/063,946

PRIOR PILING DATE: 1998-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity 24.9%; Pred. No. 1.5e-21;
Matches 98; Conservative 58; Mismatches 114; Indels 124; Gaps
                                                                                                                                                                                                                                                                               66; Mismatches 123; Indels 104; Gaps
                                                                                                                                                                                                                                       Query Match 15.7%; Score 313; DB 4; Length 1480;
Best Local Similarity 25.1%; Pred. No. 5.9e-22;
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PRIOR APPLICATION NUMBER: 60/063,946 PRIOR FILLING DATE: 1997-10-31 PRIOR APPLICATION NUMBER: 60/096,420 PRIOR FILLING DATE: 1998-08-13
                                                                                                                                                                            ORGANISM: Drosophila melanogaster
                                                                           NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO
LENGTH: 1480
                                                                                                                                                                                                                                                                                 98; Conservative
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SEQ ID NO 2
                                                                                                                                                                                                   US-09-182-024A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-182-024A-2
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                                                                                                                                                             TYPE: PRT
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|:| :|: 309 TLRLHSNHLYCDCHLAWLSDWLRQRRTVGQFTLCMAPVHLRGFNVADVQKKEYVCPAPHS 268
                                                                                                                                                                            154 RGITDVKNLO-----LDNNHISCIEDGAFRALRDLEILTLNNNNISRILVTSFNHMPKIR 208
                                                                                                                                                                                                              ------ 230
                                                                                                                                                                                                                                                                                                           269 EPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIVEIRLEQNSIKAIPAGAFT 328
                                                                                                                                                                                                                                                                                                                                                             262 RYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSGLPE-LKYLQIIFLHS 320
                                                                                                                                                                                                                                                                                                                                                                                   134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKS---LAELRIHENKVKKIQKDTF 190
                                                                                         -----LTSVPKGLPPTLLELHLDYNKISTVELEDFK 261
74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
                             34 CPTKCTCSAASVDCHGLGLRAVPRGIPRNAERLDLDRNNITRITKMDFAGLKNLRVLHLE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08986485
Fatent No. 6046030
GENERAL INFORMATION:
PAPLICANT: WU SHICK ALMOND
APPLICANT: TRUNEH, ALEMSEGED
TITLE OF INVENTION: A HUMAN LIG-1 HOMOLOG (HLIG-1)
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAINER & PRESTIA
STREET: PO. BOX 980
CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 NSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVK 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     389 NKINCLRVNTF-----QDLQNLNLLSLYDNKLQ 416
                                                                                                                                             191 KGMNALHVLEMSANPLDNNG---IEPGAFEG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,448
FILING DATE: 22-SEP-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 610-407-0700
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      610-407-0701
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29,959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :|| || :: : || || 511 LSLRNNSLQTFSPQPGLER 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 ISLFNNPVKYWEMQPATFR 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MURASHIGE, KATE H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 603 amino acids amino acids
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ADDRESSEE: Morrison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: ZVVV
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ZIP: 20006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 33
US-08-477-346-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   277 NSGSLYGLTALHQLHLSNNSISRIQRDGWSFC-----QKLHELILSFNNLTRLDEESL 329
                                                                                                                      74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
                                                                                                                                             134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEI---PLNLPKSLAELRIHENKVKKIQKDTF 190
                                                                                                                                                                                                                            103 SNELTAI-PSLGTASIGVVSLFLQHNKILSVDGSQLKSYLSLEVLDLSSNNITEIRSSCF 161
                                                                                                                                                                                                                                                                              191 KGMNALHVLEMSANPLDNNGI ---EPGAFEGV --TVFHIRLAEAKLTSVP-KGLP-PTLL 243
                                                                                                                                                                                                                                                                                                                                                                                        217 QLDLNRNRIRLIEGLIFQGLDSLEVLRLQRNNISRLTDGAFWGLSKMHVLHLEYNSLVEV 276
                                                                                                                                                                                                                                                                                                                                                                                                                                        304 PSG-LPELKYLQIIFLHSNSIARVGVN--DFCPTVPKMKKSLYSAISLFNNPVKYWEMQP 360
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                           244 ELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKI 303
                                         14.9%; Score 296; DB 3; Length 1091; 30.1%; Pred. No. 1.8e-20; tive 64; Mismatches 124; Indels 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Mochly-Rosen, Daria
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Dehlinger & Associates P.O. Box 60850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 50, Application US/08190802A Patent No. 5519003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Fabian, Gary R. REGISTRATION NUMBER: 33,875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 50:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            603 amino acids
                                                                               94; Conservative
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ADDRESSEE: Dehlinger
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                                                            Local Similarity
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US-08-190-802A-50
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US-08-986-485-5
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                                           Query Match
                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                  279 AGLMEDTFPGLLGLHVLRLAHNAIASLRPRTFKDLHFLEELQLGHNRIRQLGERTFEGLG 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195 ALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAK---LTSVP----KGLPPTLLELHL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 DYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIP--- 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    394 EHSCLGHVRLHTFAGLSGLRRLFLRDNSISSIEEQSLAGLSELLELDLTTNRLTHLPRQL 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      454 FQGLGHLEYL----LLSYNQLTTLSAEVLGPLQRAFWLDISHNHLETLAEGLFSSLGRVRY 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----VPKMKKSLYSA----
                                                                                                                        Length 603;
                                                                                                               Query Match 13.7%; Score 272; DB 1; Length 60: Best Local Similarity 28.2%; Pred. No. 1.8e-18; Matches 90; Conservative 57; Mismatches 108; Indels
; INDIVIDUAL ISOLATE: Insulin-like growth factor bind.; INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33 US-08-190-802A-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 -SGLPELKYLQIIFLHSNSIARVGVNDFCPT----
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2000 Pennsylvania Avenue, NW
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07-JUN-1995
N: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 EHSCLGHVRLHTFAGLSGLRRLFLRDNSISSIEEQSLAGLSELLELDLTTNRLTHLPRQL 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 -SGLPELKYLQIIFLHSNSIARVGVNDFCPT-----VPKMKKSLYSA----- 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---LAELRIHENKVKKIQKDTFKGMN 194
                                                                                                                                                                                                                                                                                                                                                              195 ALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAK---LTSVP----KGLPPTLLELHL 247
                                                                                                                                                                                                                                                                                                                                                                                                                               248 DYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIP--- 304
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                         102 DTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQL 161
                                                                                                                                                                                         64;
                                                                                                                                                   13.7%; Score 272; DB 4; Length 603; 28.2%; Pred. No. 1.8e-18;
                                                                                                                                                                                         Indels
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Patent No. 6342368
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
                                                                                 Insulin-like growth factor bind pro. complex-rat, Fig. 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.25
                                                                                                                                                                                     57; Mismatches 108;
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07-JUN-1995
07-JUN-1995
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2000 Pennsylvania Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PAtentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIF: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-1500
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|| || :: : || || 529
511 LSLRNNSLQTFSPQPGLER 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    346 ISLFNNPVKYWEMQPATFR 364
                                                                                                                                                                                         Conservative
              MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                              ) ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE:
; INDIVIDUAL ISOLATE:
US-08-477-346-50
TOPOLOGY: unknown
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                                                                                                                                                                   Best_Local Similarity
Matches 90; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-473-089-50
                                                 ANTI-SENSE:
                                                                                                                                                                                                                                                                                           162 SEI---
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                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    339 QLEVLTLNDNQITE--VRVGAFSG--LFNVAVMNLSGNCLRSLPERVFQGL-DKLHSLHL 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          454 FQCLGHLEYL---LLSYNQLTTLSAEVLGPLQRAFWLDISHNHLETLAEGLFSSLGRVRY 510
                                                                                                                                                                                                                                                                                                                                                                                                                                 ---PLNL------PKS-----LAELRIHENKVKKIQKDTFKGMN 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 DYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIP--- 304
                                                                                                                                                                                                                                                                                                                                           102 DTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQL 161
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 -SGLPELKYLQIIFLHSNSIARVGVNDFCPT------VPKMKKSLYSA----
                                                                                                                                                                                                                                                                                               64;
                                                                                                                                                                                                                                                Length 603;
                                                                                                                                                                                                                                                13.7%; Score 272; DB 4; Length 603
28.2%; Pred. No. 1.8e-18;
tive 57; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorin
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
                                                                                                                                                          INDIVIDUAL ISOLATE: Insulin-like growth factor bind. INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
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07-JUN-1995
N. F.
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STREET: 2000 Pennsylvania Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 50, Application US/08487072A Patent No. 6423684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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511 LSLRNNSLQTFSPQPGLER 529
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: 603 amino acids
amino acid
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                                                                   protein
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 90; Conserval
                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington
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                                            TOPOLOGY: un}
                                                                                                             ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                      HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-487-072A-50
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                                                                                                                                                                                                      US-08-473-089-50
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LENGTH:
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260 VNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSLAVDNLPDLRKIEATNN 319
                                                                                                                                                                                                                                                                                                                                                                                         149 HNLLSTISPGAFIGL-HNLLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMN 207
                                                                                                                                                                                                                                   208 -FKP-----LINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPHVALQKV 259
                                                                89 DFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLEENKLTELPEKCLSELSNLQELYIN 148
                                                                                                          158 HNQLSEIP----LNLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPL----DNN 209
                                                                                                                                                                                                                                                                               245 ----LHLDYNKISTVELEDFKRYKELQRLGLGN-NKITDIENGSLANIPRVREIHLENN 298
                                                                                                                                                                                                                                                                                                                                                                 299 -KLKKI-PSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVK-- 354
                      ---KGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.0%; Score 259.5; DB 3; Length 1101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SWEET, RAYMOND
APPLICANT: TRUNEH, ALEMSEGED
TITLE OF INVENTION: A HUMAN LIG-1 HOMOLOG (HLIG-1)
                                                                                                                                                                                             210 GIEPGAFEGVTVFHIR---IAEAKLTSVPKG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UMBER: US/08/986,485
08-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          374 CVIRWMNMNKTNIRFMEPDSLFCV 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08986485 Patent No. 6046030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23,031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 846169
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 22-SEP-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1101 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    610-407-0700
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REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: P.O. BOX 980 CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                        120 DF-
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                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                           219 ELRELDLSRNALRSVKANVFVHLPRLQKLYLDRNLITAVAPGAFLGMKALRWLDLSHNRV 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339 QLEVLLINDNQITE--VRVGAFSG--LFNVAVMNLSGNCLRSLPERVFQGL-DKLHSLHL 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 -SGLPELKYLQIIFLHSNSIARVGVNDFCPT------VPKMKKSLYSA----- 345
                                                                                                                                                                                                                                                                                                                                                               102 DTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                162 SEI------PLNL-----PKS-----LAELRIHENKVKKIQKDTFKGMN 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      279 AGLMEDTFPGLLGLHVLRLAHNAIASLRPRTFKDLHFLEELQLGHNRIRQLGERTFEGLG 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 ALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAK---LTSVP----KGLPPTLLELHL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 DYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIP--- 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 CPFGCQCYSR-------VVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIK-EN 119
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                                                                                                                                                                                                                                                                         13.7%; Score 272; DB 4; Length 603; 28.2%; Pred. No. 1.8e-18; Live 57; Mismatches 108; Indels
                                                                                                                                                                                         Insulin-like growth factor bind. pro. complex-rat, Fig. 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: EXTRACELLULAR ADHESIVE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/131,648 US/08/18 FILING DATE: 1998-08-10 NUMBER OF SEQ ID NOS: 5 SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09131648 Patent No. 6168920
    50:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|| || :: : || || 529
511 LSLRNNSLQTFSPQPGLER 529
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 603 amino acids
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                                                                                                                                                                                                                                                                                                                     90; Conservative
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US-09-131-648-2
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                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                   ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                        unknown
                                                                amino acid
                                                                                                                                                                                                                                                                                                 Local Similarity
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N
                                                                                   TOPOLOGY:
                                                                                                                                                   ANTI-SENSE:
                                                                                                                                                                                                                                   US-08-487-072A-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-131-648-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 2
LENGTH: 708
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Best Local S
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52 CTCAGDSLDCGGRGLAALPGDLSWTRSLNLSYNKLAEIDPAGFEDLPNLQEVYLNNHEL 111
                                                                                                                                                                                                                                                         148 ------NLPKSLAELRIYLSHNQLSEIPL---NLPKSLAELRIHENKV 182
                                                                                                                                                                                                                                                                                    172 IKELNLAGNRIGTLELGAFDGLSRSLLTLRLSKNRITQLPVRAFKLPR-LTQLDLNRNRI 230
                                                                                                                                                                                                                                                                                                                                                    183 KKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHI-RIAEAKLTSVPKGL--- 238
                                                                                                                                                                                                                                                                                                                                                                                    239 PPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENN 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 LTALHQEHLSNNSIARIHRKGWSFCQKLHELVLSFNNLTRLDEESLAELSSLSVLRLSHN 348
                        85; Gaps
                                                                  78 CQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKL 137
                                                                                                                                                                ---- 147
                                                                                                                                                                                                            112 TAVASLGAGSSQVVALFLQQQQNRSLDGSQLKAYLSLEVLDLNLNITEVRNTYFPHGPP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : | | | : | | : | | : | 349 SISHIAEGAFKGLRSLRVLDLDHNEISGT-IEDTSGAFSGLEFG-HSKLTLFGNKIK 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 KLKKIPSG-LPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVK 354
23.2%; Pred. No. 7.6e-17;
iive 69; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: RUOSICHIT, ERKKI I.
APPLICANT: PIERSCHBACHER, MICHAEL D.
APPLICANT: CARDISMS, JOSE
APPLICANT: CARLISM, MILLIAM
APPLICANT: MULLEN, DANIEL G.
TITLE OF INVENTION: DECORIN FRACMENTS AND METHODS OF
TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,063A
FILING DATE: 16-MAX-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,652
ATION DATE: 03-APR-1992
ATIONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEE: CAMPBELL AND FLORES: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700 SAN DIEGO
                                                                                                                                                                  ---HPKAFLT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 33, Application US/08442063A
Patent No. 5705609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 31,815
REPERBICE/COCKET UNBER: P-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAMPBELL, CATHRYN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CALIFORNIA
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  Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 SLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNL---PKSLAELRIHENKV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 DEDNSLFPTREPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQ 109
                                                          1; Gaps
                                                                                                        32;
                        12.9%; Score 256.5; DB 1; Length 96; 54.8%; Pred. No. 4.1e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.8%; Score 254; DB 3; Length 353; 28.1%; Pred. No. 5e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: WU, SHUJIAN
APPLICANT: SWEET, RAYMOND
APPLICANT: TRUNEH, ALEMSEGED
TITLE OF INVENTION: A HUMAN LIG-1 HOMOLOG (HLIG-1)
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/986,485 FILLING DATE: 08-DEC-1997
                                                          13; Mismatches
                                                                                                                                                         110 NNKIKEIKENDFKGLTSLYGLILNNNKLTKIHP 142
                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,448
FILING DATE: 22-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
                                                                                                                                                                                                                                                                         Sequence 6, Application US/08986485 Patent No. 6046030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23,031
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      610-407-0700
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-986-485-6
                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: P.O. BOX 980
CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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US-08-442-063A-33
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                                                             51;
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                                                                                                                                                                                                                                             RESULT 39
US-08-986-485-6
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                              Query Match
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                                                            Matches
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Db 99 SLGFLNLQGGQLGSLEPQALLGLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRL 156		Db 159 SRLEDGLFEGLGSLWDLNLGWNSLAVLPDAAFRGL	OY 242 LIELHLDYNKISTVELEDFKRYKELQRIGLGNNKITDIENGSLANIPRVREIHLENNKLK 30	Db 196 IRELVLAGNRLAYLQPALFSGLAELRELDLSRNALRANVFVQLPRLQKLYLDRNLIA 259	302	Db 256 AVAPGAFLGLKALRWLDLSHNRVAGL-LEDTFPGLLGLRVLRLSHNAIASLRP 307	361	Db 308 RTFKDLHFLEELQLGH 323	RESULT 41	.Sequence 49, Application US/08477346	GENERAL INFORMATION:  ADDITORMY MACHIN-Docon Daria	with the second	; TILLE OF INVENTION: MO 40 Delived Peptides and USES ; TILLE OF INVENTION: Thereof ; NIMBER OF SPOITEMPES: 265	CORRESPONDENCE ADDRESS:	STREET: 2000 Pennsylvania Avenue, NW	ä ö	; COUNTRY: USA ; ZIP: 20006-1812	COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk	IBM PC compatible SYSTEM: PC-DOS/MS-DOS	In F DAT	: APPLICATION NUMBER: US/08/477,346 : FILING DATE: 07-JUN-1995	CLASSIFICATION: 514 PRIOR APPLICATION DATA:	; APPLICATION NUMBER: 08/487,072 ; FILING DATE: 07-JUN-1995	; ATTORNEY/AGENT INFORMATION: ; NAME: MURASHIGE, KATE H	TRATION NUMBER: 29,959	21	TELEPHONE: (202) 887-1500	SECOND FOR SEQ ID NO: 49:	: LENGTH: 605 amino acid	; TOPOLOGY: unknown ; MOLECULE TYPE: protein	HYPOTHETICAL: NO ANTI-SENSE: NO OPTIGINAL SOUTER	DIVII	-49	3%; Score 246; DB 4; Length 605; 3%; Pred. No. 6.8e-16;	aa ccii	1 0y 72 PMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLT 125
Qy 183 KKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFH-IRIAEAKLTSVPKGLPPT 241	Db 124 GRLEEGLFOGLSHLWDLNLGWNSLVVLPDTVFQGLGNLHELVLAGNKLTYLQPA 177	OY 242 LLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIH 294		295 LENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSALSLFNNP	DO 238 LSHNKVAGLMEDTFPGLLGLHVLRLAHNAIASLRPRTFRDLHFLEELQLGHNR 290 OV 353 VK 354		DD 291 IR 292	RESULT 40 US-08-190-802A-49	; Sequence 49, Application US/08190802A ; Patent No. 5519003	; GENERAL INFORMATION: ; APPLICANT: Mochly-Rosen. Daria	<pre>; APPLICANT: Ron, Dorit ; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses</pre>	; TITLE OF INVENTION: Thereof ; NUMBER OF SEQUENCES: 265	CORRESPONDENCE ADDRESS: ADDRESSEE: Dehlinger & Associates	; STREET: P.O. Box 60850 ; CITY: Palo Alto		21F: 94306-0850 COMPUTER READABLE FORM:	MEDIUM TYPE: Floppy disk	O)	40	<u> </u>	5.5	TRATION NU	TELECOMUNICATION INCREM. 0000 0139 TELECOMUNICATION 10000 TELECOMUNICATION 10000	; TELEFAX: (*15) 324 -0060	SEQUENCE CHARACTERISTICS: 49:	; LENGTH: 605 amino acids ; TYPE: amino acid	; TOPOLOGY: unknown ; MOLECULE TYPE: protein	; HYPOTHETICAL: NO ; ANTI-SENSE: NO	Thenlin-libo assemble factor to be	// INDIVIDUAL ISOLATE: protein complex, Fig. 32	Query Match 12.3%; Score 246; DB 1; Length 605;	25.3%; Pred. No. 6.8e-16; vative 61; Mismatches 133;	QY 72 PMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLT 125	39		

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9.
                                  KKIQKDTFKGMNALHVLEMSANPLDNNGIEP-GAFEGVTVFHIRIAEAKLTSVPKGLPPT 241
                                                                                                                                                .RELVLAGNRLAYLQPALFSGLAELRELDLSRNALRAIKANVFVQLPRLQKLYLDRNLIA 255
                                                                                                                                                                                                    (I-PSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQP 360
SIGFLNLQGGQLGSLEPQALLGLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRL 158
                                                                                    -----GS 195
                                                                                                                  JELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLK 301
                                                                                                                                                                                                                                th 12.3%; Score 246; DB 4; Length 605; Similarity 25.3%; Pred. No. 6.8e-16; B0; Conservative 61; Mismatches 133; Indels 42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /IDUAL ISOLATE: Insulin-like growth factor binding IDUAL ISOLATE: protein complex, Fig. 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CANT: Mochly-Rosen, Daria
CANT: Ron, Dorit
OF INVENTION: WD-40 - Derived Peptides and Uses
OF INVENTION: Thereof
OF SEQUENCES: 265
SPONDENCE ADDRESS:
                                                                  SRLEDGLFEGLGSLWDLNLGWNSL---AVLPDAAFRGL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TER READABLE FORM:
TER READABLE FORM:
IUM TYPE: Floppy disk
FURTER: IBM PC compatible
RATING SYSTEM: PC-DOS/MS-DOS
TWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NG DATE: 07-JUN-1995

HEY/AGENT INFORMATION:
1: MURASHIGE, KATE H.
STERATION NUMBER: 29,959

SRENCE/DOCKET NUMBER: 2550-0025.20

MMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESSEE: Morrison & Foerster
NET: 2000 Pennsylvania Avenue, NW
: Washington
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ICATION NUMBER: US/08/477,346
ING DATE: 07-JUN-1995
SSIFICATION: 514
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  49, Application US/08477346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08/487,072
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SIEFAX: (202) 887-1500
SIEROS EQUID NO: 49:
ENCE CHARACTERISTICS:
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amino acid
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                                                                                                                                                                                                                                                                                                                           TFKDLHFLEELQLGH 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
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                                                                                                                                                                                                                                                                                                                                                                                                               46-49
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159 SRLEDGLFEGLGSLWDLNLGWNSL---AVLPDAAFRGL-------GS 195
                                                                                                                                                                                                                                                                                                                                            302 KI-PSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQP 360
                                                                                                                                                                                                                                                                                                                                                                         196 LRELVLAGNRLAXLQPALFSGLAELRELDLSRNALRAIKANVFVQLPRLQKLYLDRNLIA 255
      72 PMCPFGCQCY----SRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLT 125
                                                                                          126 SLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNL---PKSLAELRIHENKV 182
                                                                                                                         183 KKIQKDTFKGMNALHVLEMSANPLDNNGIEP-GAFEGVTVFHIRIAEAKLTSVPKGLPPT 241
                                                                                                                                                                                                                                                             242 LLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLK 301
                                   39 PACPAACVCSYDDDADELSVFCSSRNLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLS 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit-1
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION UNDBER: 29,959
REPERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.3%; Score 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2: Morrison & Foerster
2000 Pennsylvania Avenue, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-487-072A-49; Sequence 49, Application US/08487072A; Patent No. 6423684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 49:
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NO
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; INDIVIDUAL ISOLATE:
US-08-487-072A-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
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ANTI-SENSE: N
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                                                           126 SLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNL---PKSLAELRIHENKV 182
                                                                                                     99 SLGFLNLQGGQLGSLEPQALLGLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRL 158
                                                                                                                                               183 KKIQKDTFKGMNALHVLEMSANPLDNNGIEP-GAFEGVTVFHIRIAEAKLTSVPKGLPPT 241
                                                                                                                                                                                    159 SRLEDGLFEGLGSLWDLNLGWNSL---AVLPDAAFRGL--------GS 195
                                                                                                                                                                                                                              242 LLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLK 301
                                                                                                                                                                                                                                                                    196 LRELVLAGNRLAYLQPALFSGLAELRELDLSRNALRAIKANVFVQLPRLQKLYLDRNLIA 255
                                                                                                                                                                                                                                                                                                                                        133; Indels 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
UNDBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
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....... US/08/473,089
07-JUN-1995
7N: 435
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6342368
GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
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TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
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NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,
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Best Local Similarity 25.3%
Matches 80; Conservative
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FILING DATE: 07-JUN
CLASSIFICATION: 435
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20006-1812
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TITLE OF INVENTION: A HUMAN LIG-1 HOMOLOG (HLIG-1) NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS:
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,485
FILLING DATE: 08-DEC-1997
                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/063,950C CURRENT FILING DATE: 1998-04-21 NUMBER OF SEO ID NOS: 9 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 CPFGCQC-YSRVVHCSDLGLTSVPTNIPFDT--
                                                                                                     : Sequence 2, Application US/09063950C
; Patent No. 6225085
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WU, SHUJIAN
SWEET, RAYMOND
TRUNEH, ALEMSEGED
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.1%
Best Local Similarity 28.5%
Matches 85; Conservative
         308 RTFEDLHFLEELQLGH 323
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                                                                                                                                                                                                                  FILE REFERENCE: MEI-019
                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                               SEQ ID NO 2
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TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
CURRENT APPLICATION NUMBER: US/09/063,950C
CURRENT APPLICATION NUMBER: US/09/063,950C
NUMBER OF SEQ ID NOS: 9
SOFWARE: Patentin Ver. 2.0
SEQ ID NO 5
                                                 72 PMCPFGCQCY----SRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLT 125
                                                                                                                            126 SLYGLILUNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNL---PKSLAELRIHENKV 182
                                                                                                                                                              99 SLGFLNLOGGQLGSLEPQALLGLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRL 158
                                                                                                                                                                                                                              183 KKIQKDTFKGMNALHVLEMSANPLDNNGIEP-GAFEGVTVFHIRIAEAKLTSVPKGLPPT 241
                                                                                                                                                                                                                                                                               242 LLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLK 301
                                                                                                                                                                                                                                                                                                         302 KI-PSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQP 360
                                                                                                                                                                                                                                                                                                                                                                                ; Pred. No. 6.8e-16;
61; Mismatches 133; Indels 42; Gaps
                                                                                       39 PACPAACVCSYDDDADELSVFCSSRNLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLS 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 605;
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12.1%; Score 241; DB 4; Length 605
Best Local Similarity 26.3%; Pred. No. 2.1e-15;
Matches 83; Conservative 59; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 5, Application US/09063950C
; Patent No. 6225085
 25.3%;
                 80; Conservative
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Best Local Similarity
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               Matches
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APPLICANT: HOLTZMAN, DOUGLAS A. TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES TITLE OF INVENTION: THEREFOR
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28.5%; Pred. No. 2.5e-15;
Live 51; Mismatches 108; Indels 54; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---RMLDL 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 LNLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIR 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 IAEAKLTSVPKGLPPTLLELH-LDYNKISTVELED----FKRYKELQRLGL-GNNKITDI 279
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: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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Fri Jan 24 13:09:53 2003

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74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
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-------QLYLHFNQIE 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 NNQIKRIPSGAFEDLENLKYLYL-------YKNEIQSIDRQAFKGL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             68;
                                                                                                                                                                                                                                                                                                                                                                                                    / Match 12.0%; Score 239; DB 3; Length 180; Local Similarity 25.6%; Pred. No. 5.6e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                               58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 TVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: CALLey, Neil C
APPLICANT: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYSTEM: DOS FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                 43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                    GH-70264
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,448
FILING DATE: 22-SEP-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08985335
Patent No. 6080847
                                                                         NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                                                                                                                                  TELEX: 846169
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                               180 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                 58; Conservative
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                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-986-485-8
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                                                                                                                                                                                                                                                                                    amino acid
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214 -----GAFEGVTVFHIRIAEAK---LTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKE 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 TLISMLOIPRNRNLGNYAKCESPQEQKNKKLRQIKSEQLCNEEKEQLDPKPQVSGRPPVI 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 KPEVDSTFCHNYVFPIQTLDCKRKELKKVPNNIPPDIVKLDLSYNKINQLRPKEFEDVHE 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 CDVYTYLHEKYLDCQERKLVYVLPGWPQDLLHMLLARNKIRTLKNNMFSKFKKLKSLDLQ 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52; Mismatches 117; Indels 54; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 LQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSG-LPELKYLQIIFLHSN 321
                                                                                                                                                                                                                                                                                                                                          11.8%; Score 236; DB 3; Length 440; 24.9%; Pred. No. 4.2e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 -----KVKKIQKDTFKGMNALHVLEMSANPLDNNGIEP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SE: Incyte Pharmaceuticals, Inc.
3174 Porter Dr.
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION: TELECOMMUNICATION: 650-855-0555
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09410372 Patent No. 6281334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hillman, Jennifer L.
                                                                                TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 24.99
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yue, Henry
Lal, Preeti
Shah, Purvi
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                     STRANDEDNESS: single
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                                                                                                                                                                                                                                                              ; LIBRARY: LATRIUT02
; CLONE: 1352286
US-08-985-335-3
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CTTY: Palo Alto
                                                                                                                                                                                                                             linear
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APPLICANT:
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APPLICANT: Rothberg, Jonathan Marc and Artavanis-Tsakonas, Spyridon
TITLE OF INVENTION: Purified SLIT protein and Sequence Elements Thereof
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 CQCYS----RVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 NNKLTKIHPKAFLTTKKLRRLYLSHNQL----SEIPLNLPKSLAELRIHEN----- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 CDVYTYLHEKYLDCQERKLVYVLPGWPQDLLHMLLARNKIRTLKNNMFSKFKKLKSLDLQ 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 ONEISKIESEAFFGLNKLTTLLLQHNQIKVLTEEVFIYTP-LLSYLRDNPWHCTCEIE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 ----- KVKKIQKDIFKGMNALHVLEMSANPLDNNGIEP----- 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 ----GAFEGVTVFHIRIAEAK---LTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKE 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 TLISMLQIPRNRNLGNYAKCESPQEQKNKKLRQIKSEQLCNEEKEQLDPKPQVSGRPPVI 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 KPEVDSTECHNYVPPIQTLDCKRKELKKVPNNIPPDIVKLDLSYNKINQLRPKEFEDVHE 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266 LQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSG-LPELKYLQIIFLHSN 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.8%; Score 236; DB 4; Length 440; Best Local Similarity 24.9%; Pred. No. 4.2e-15; Matches 74; Conservative 52; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette, 3.50 inch. 800 Kb storage COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintosh 6.0.5 SOFTWARE: Microsoft Word 4.0 SOFTWARE: Microsoft Word 4.0 Application DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yale University
ADDRESSEE: Office of Cooperative Research
STREET: 246 Church Street
STREET: Suite 401
                    NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US91/09055 FILING DATE: 19911127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/624,135
FILING DATE: 7-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barth, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application PC/TUS9109055 GENERAL INFORMATION:
                                                                                                                                             TELEFAX: 650-845-4166 INFORMATION FOR SEQ ID NO: 3:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                 LIBRARY: LATRIUT02
CLONE: 1352286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Connecuticut
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APPLICANT: James Gilmore
APPLICANT: James Gilmore
APPLICANT: James Gilmore
APPLICANT: Laura Stuve
TITLE ON INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL
TITLE OF INVENTION: PROLIFERATION
FILE REPERENCE: PA-0003 US
CURRENT APPLICATION NUMBER: US/09/232,160
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PELL PROGRAM
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 KGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYN 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 KISTVELEDFKRYKELQRLGLONNKITDIENGSLANIPRVREIHLENNKLKKIPSGLP-- 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 309 ---ELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRC 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                          11.1%; Score 222; DB 5; Length 224; 22.3%; Pred. No. 3.8e-14; Live 49; Mismatches 89; Indels 10
                                                                                                                                                                                                                                                                                                                         : IDENTIFICATION METHOD: similarity to other Flank-LRR-OTHER INFORMATION: mediates adhesive events
PCT-US91-09055-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CPHPCRCADGIVDCREKSLTSVPVTLPDDTTDVRLEQNFI---
REGISTRATION NUMBER: 28,180
REFERENCE/DOCKET NUMBER: 900964/RSB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 972-1400
TELEFAX: (212) 370-1622
TELEFAX: 236.268
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/09232160 Patent No. 6368794
                                                                                                                                                                                                                                                                                         NAME/KEY: Flank-LRR-Flank 2
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 22,3%
Matches 69; Conservative
                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: 159452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                           Linear
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                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-232-160-17
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10.7%; Score 212.5; DB 4; Length 298;

Query Match

Bes	Best Local Similarity 27.5%; Pred. No. 5e-13; Matches 74; Conservative 41; Mismatches 101; Indels	ls 53; Gaps	10;
Qy	51	PFDTRMLDLQN 110	
QQ	Db 75 KDEAITPLPPKKENDEMPTCLL-CVCLSGSVYCEEVDIDAVPP-LPKESAYLYARF 128	PKESAYLYARF 128	_
Qy	QY 111 NKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPK 170	QLSEIPLNLPK 170	-
qq		OLLKLPV-LPP 187	
QY	171	GUTVFHIRIAE 228	
qq	DD 188 KLTLFNAKYNKIKSRGIKANAFKKLNNLTFLYLDHNALE226	226	10
Qy	229	DIENGSLANIP 288	m
qq	227SVPLNLPESLRVIHLQFNNIASITDDTFCKANDT	SYIRD 265	10
δλ	QY 289 RVREIHLENNKLKKIPSGLPELKYLQI 315		
qq	266		
Sear	Search completed: January 24, 2003, 12:27:03 Job time : 24 secs		

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein January 24, 2003, 12:26:46; Search time 12 Seconds (without alignments) 637.306 Million cell updates/sec Run on:

Perfect score:

US-09-944-457-2 1992 1 MKEYVLLIFLALCSAKPFFS......PATFRCVLSRMSVQLGNFGM 379 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

122226 seqs, 20178551 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Published\_Applications\_AA:\* Database :

1: //cgn2\_6/ptodata/2/pubpaa/USOB\_NEW\_PUB.pep:\*
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
3: /cgn2\_6/ptodata/2/pubpaa/USO6\_NEW\_PUB.pep:\*
4: /cgn2\_6/ptodata/2/pubpaa/USO6\_PUBCOMB.pep:\*
5: /cgn2\_6/ptodata/2/pubpaa/USO6\_PUBCOMB.pep:\*
6: /cgn2\_6/ptodata/2/pubpaa/USO7\_PUBCOMB.pep:\*
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14: /cgn2\_6/ptodata/2/pubpaa/USO9\_NEW\_PUB.pep:\*
14: /cgn2\_6/ptodata/2/pubpaa/USO0\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Sequence 2, Appli	Sequence 328, App	Sequence 2, Appli																	
	ID	US-09-944-413-2	US-09-944-403-2	US-09-944-896-2	US-09-944-944-2	US-09-944-907-2	US-09-944-929-2	US-10-028-072-328	US-09-866-028-2	US-09-944-449-2	US-09-944-457-2	US-09-944-862-2	US-09-945-587-2	US-09-945-015-2	US-09-944-396-2	_	US-09-944-432-2	US-09-943-762-2	US-09-944-654-2	US-09-943-851A-2	
	DB	- 6	6	6	σ	0	6	6	10	10	10	10	10	10	10	10	10	10	10	10	
	Query Match Length DB	379	379	379	379	379	379	379	379	379	379	379	379	379	379	379	379	379	379	379	
dР	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
	Score	1992	1992	1992	1992	1992	1992	1992	1992	1992	1992	1992	1992	1992	1992	1992	1992	1992	1992	1992	
	Result No.		7	3	4	S	9	7	89	6	10	11	12	13	14	15	16	17	18	19	

Sequence 1561, Ap	sednence 300, App	Sequence 302, App	Sequence 36, Appl	Sequence 276, App	Sequence 132, App	Sequence 6, Appli	Sequence 384, App	Sequence 384, App	Sequence 132, App	Sequence 384, App	Sequence 132, App	Sequence 384, App	Sequence 370, App	Sequence 1192, Ap	Sequence 28, Appl	Sequence 115, App	Sequence 28, Appl	Sequence 28, Appl	Sequence 28, Appl	Sequence 28, Appl	Sequence 350, App	Sequence 28, Appl	Sequence 28, Appl	Sequence 5, Appli	Sequence 290, App	Sequence 290, App	Sequence 290, App	Sequence 2, Appli	Sequence 290, App	Sequence 124, App
US-09-925-301-1561	086-T08-975-80	US-10-028-072-302	US-10-028-072-36	US-09-764-870-276	US-10-063-547-132	US-10-004-551-6	US-10-174-590-384	US-10-176-758-384	US-10-063-616-132	US-10-175-737-384	US-10-006-867-132	US-10-052-586-384	US-10-028-072-370	US-09-925-301-1192	US-09-905-291A-28	US-10-066-500-115	US-09-902-853-28	US-09-907-824-28	US-09-907-841-28	US-09-904-011-28	US-10-028-072-350	US-09-909-320-28	US-09-909-088B-28	US-10-011-064-5	US-10-174-590-290	US-10-176-758-290	US-10-175-737-290	US-10-011-064-2	US-10-052-586-290	US-10-063-547-124
10	10	σ	6	10	σ	6	5	6	5	6	12	12	6	10	6	6	σ	6	6	6	6	10		12	6	6	Φ	12	12	δ
155	353	421	674	623	649	649	649	649	649	649	649	649	642	415	099	099	099	099	099	099	099	099	099	1480	1523	1523	1523	1523	1523	513
20.4	19.7	18.4	18.2	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.5	16.2	15.7	15.7	15.7	15.7	15.7	15.7	15.7	15.7	15.7	15.7	15.5	15.5	15.5	15.5	15.5	15.3
406.5	393	366	363,5	331.5	331.5	331.5	331.5	331.5	331.5	331.5	331.5	331.5	329	323	313.5	313.5	313.5	313.5	313,5	313.5	313.5	313.5	313.5	313	309	309	309	309	309	304.5
20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	4	41	42	43	44	4.5	46	47	4.8	4.9	20

## ALIGNMENTS

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ATTLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC; TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P5548P1C1

CURRENT APPLICATION NUMBER: US/09/944,413

CURRENT FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-06-26

PRIOR FILING DATE: December 3, 1997

PRIOR PILING DATE: December 11, 1997

PRIOR PILING DATE: December 11, 1997

PRIOR FILING DATE: December 11, 1997

PRIOR PILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,278

PRIOR APPLICATION NUMBER: 60/069,278

PRIOR APPLICATION NUMBER: 60/069,278
                                     Sequence 2, Application US/09944113
Patent No. US20020156004A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
Kljavin, Ivar
Napier, Mary
Roy, Margaret
Tumas, Daniel
                                                                                                                                                                                    Ferrara, Napoleone
Filvaroff, Ellen
                                                                                                                                     Botstein, David
                                                                                                                                                                                                                                   Gerritsen, Mary
Goddard, Audrey
                                                                                                               APPLICANT: Baker, Kevin
                                                                                                                                                                Eaton, Dan
RESULT 1
US-09-944-413-2
                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                APPLICANT:
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APPLICANT:
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                                                                                                                                                                APPLICANT:
                                                                                                                                                                                    APPLICANT:
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APPLICANT:
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DB 9; Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: JULy 28, 1998
PRIOR PAPLICATION NUMBER: 60/146,222
PRIOR PELING DATE: SUPPLICATION NUMBER: PCT/USS8/19330
PRIOR FILING DATE: SEPTEMBER: PCT/USS8/25108
PRIOR FILING DATE: December 16, 1998
PRIOR PILING DATE: December 1, 1998
PRIOR PLING DATE: December 12, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR PILING DATE: December 22, 1998
PRIOR PLING DATE: MARCH 3, 1999
PRIOR PAPLICATION NUMBER: PCT/US99/1255
PRIOR PAPLICATION NUMBER: PCT/US99/1265
PRIOR PILING DATE: September 15, 1999
PRIOR PILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR PILING DATE: September 15, 1999
PRIOR PILING DATE: September 15, 1999
PRIOR PILING DATE: SEPTEMBER 30, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1992;
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PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: February 22, 2000
APPLICATION NUMBER: PCT/US00/05841
FILING DATE: March 2, 2000
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PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
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APPLICATION NUMBER: 60/112,850
FILING DATE: December 16, 1998
APPLICATION NUMBER: 60/113,296
                                                                                                      APPLICATION NUMBER: 60/069,694
FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,702
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APPLICATION NUMBER: 60/069,870
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APPLICATION NUMBER: 60/069,873
FILING DATE: December 17, 1997
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APPLICATION NUMBER: 60/074,086
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APPLICATION NUMBER: 60/074,092
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APPLICATION NUMBER: 60/075,945
    FILING DATE: December 12, 1997
                                         APPLICATION NUMBER: 60/069,696
FILING DATE: December 16, 1997
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US-09-944-413-2
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CURRENT APPLICATION NUMBER: US/09/944,403
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
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PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: December 11, 1997
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PRIOR FILING DATE: December 12, 1997
PRIOR PELLORIUM NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
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Patent No. US20020165143A1
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Grimaldi, Christopher
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                                  Matches 379; Conservative
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APPLICANT: Botstein, David
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                 Best Local Similarity
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PRIOR APPLICATION NUMBER: 60/069,694

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ITTLE OF INVENTION: ACIDS ENCODING THE SAME
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1 MKEYVLLIFIALCSAKPFFSPSHIALKNAMLKDMEDTDDDDDDDDDDDDDDDDSLFPTRE
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CURRENT APPLICATION NUMBER: US/09/944,896
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
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PRIOR PELLING DATE: December 11, 1997
PRIOR PELLING DATE: December 12, 1997
PRIOR PELLING DATE: December 12, 1997
PRIOR PELLING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
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PRIOR PELLING DATE: December 16, 1997
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Patent No. US20020168715A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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Grimaldi, Christopher
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Filvaroff, Ellen
Gerritsen, Mary
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Hillan, Kenneth
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US-09-944-896-2
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PRIOR FILING DATE: September 1, 1998
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PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR PELING DATE: March 3, 1999
PRIOR FILING DATE: March 3, 1999
PRIOR FILING DATE: March 3, 1999
PRIOR FILING DATE: June 22, 1999
PRIOR FILING DATE: September 15, 1999
PRIOR FILING DATE: No. US20020165143Alember 30, 1999
PRIOR FILING DATE: December 1, 1999
PRIOR FILING DATE: December 1, 1999
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100.0%; Pred. No. 2e-159;
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PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US90/03565
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR PILING DATE: February 11, 2000
PRIOR FILING DATE: February 22, 2000
PRIOR FILING DATE: PEDTUARY 22, 2000
PRIOR PELING DATE: MATCh 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08419
PRIOR PILING DATE: MATCh 3, 2000
PRIOR PLING DATE: MATCh 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR PLING DATE: MAY 22, 2000
PRIOR PLING DATE: MAY 28, 2000
PRIOR PLING DATE: JULY 28, 2000
PRIOR PLING DATE: JULY 28, 2000
PRIOR PLING DATE: JULY 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: DECEMBER: PCT/US00/32678
PRIOR PLING DATE: DECEMBER: PCT/US00/32678
PRIOR PLING DATE: DECEMBER: TCT/US00/32678
PRIOR PLING DATE: DECEMBER: TCT/US01/06520
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APPLICATION NUMBER: PCT/US98/19330
FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
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APPLICATION UNMBER: 60/113, 296
FILING DATE: December 22, 1998
APPLICATION NUMBER: 60/146,222
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APPLICATION NUMBER: 60/074,086
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APPLICATION NUMBER: 60/075,945
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APPLICATION NUMBER: 60/069,870
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FILING DATE: December 16, 1997
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APPLICATION NUMBER: 60/069,873
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PRIOR FILLNG DATE: NO. US20020168715A1ember 30, 1999
PRIOR FILLNG DATE: NO. US20020168715A1ember 30, 1999
PRIOR FILLNG DATE: NO. US20020168715A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
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PRIOR APPLICATION NUMBER: 09/218, 517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254, 311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/1252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/2090
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PRIOR PLING DATE: February 22, 2000
PRIOR FILING DATE: March 2, 2000
PRIOR PLING DATE: March 30, 2000
PRIOR PLING DATE: March 30, 2000
PRIOR PLING DATE: March 30, 2000
PRIOR PLING DATE: May 22, 2000
PRIOR PLING DATE: May 22, 2000
PRIOR FILING DATE: July 28, 2000
PRIOR FILING DATE: July 28, 2000
PRIOR PLING DATE: July 28, 2000
PRIOR PLING DATE: December 1, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: PEDFUNGINGOUSE PRIOR FILING DATE: PEDFUNGING 28, 2001
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APPLICATION NUMBER: PCT/US98/25108
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APPLICATION NUMBER: PCT/US99/30095
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APPLICATION NUMBER: PCT/US00/03565
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PRIOR APPLICATION NUMBER: PCT/US00/04414
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PRIOR APPLICATION NUMBER: 60/074,086
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR PELING DATE: February 9, 1998
PRIOR FILING DATE: February 9, 1998
PRIOR FILING DATE: February 25, 1998
PRIOR FILING DATE: February 25, 1998
PRIOR FILING DATE: DECEMBER: 60/112,850
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: DECEMBER: 22, 1998
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PRIOR APPLICATION NUMBER: PCT/US99/28
PRIOR FILING DATE: December 17, 1997 PRIOR APPLICATION NUMBER: 60/068,017 PRIOR FILING DATE: December 18, 1997 PRIOR APPLICATION NUMBER: 60/070,440
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FILING DATE: July 28, 1999
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FILING DATE: December 16, 1998
BAPING DATE: December 20,218,517
FILING DATE: December 22, 1998
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NUMBER OF SEQ ID NOS: 120
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Matches 379; Conservative
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US-09-944-896-2
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PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60,069,334
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PRIOR APPLICATION NUMBER: 60/069335
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PRIOR PELLOGICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
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PRIOR FILLING DATE: December 12, 1997
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PRIOR FILING DATE: December 16, 1997
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PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
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PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
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Grimaldi,Christopher
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APPLICANT: Botstein, David
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Hillan, Kenneth
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Eaton, Dan
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FILING DATE: No. US20020173463Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
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100.0%; Pred. No. ·2e-159;
tive 0; Mismatches 0;
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OR APPLICATION NUMBER: PCT/USO0/04414
OR FILING DATE: FEDERALY 22, 2000
OR APLICATION NUMBER: PCT/USO0/05841
OR PILING DATE: MATCH 2, 2000
OR APPLICATION NUMBER: PCT/USO0/08439
OR FILING DATE: MATCH 30, 2000
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PRIOR FILING DATE: May 22, 2000
PRIOR PLICATION NUMBER: PCT/USO0/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/USO0/32678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: December1, 1999
PAPLICATION UNMBER: PCT/USS9/30095
FILING DATE: December 16, 1999
APPLICATION NUMBER: PCT/US00/03565
                                                                                                                                                                                                                                         FILING DATE: July 28, 1999
APPLICATION NUMBER: PCT/0594/19330
FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
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APPLICATION NUMBER: PCT/US99/28409
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US99/12252
FILING DATE: June 22, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US99/21090
                                                                                                                                                                                                                                                                                                                      R FILING DATE: December 1, 1998
R APPLICATION NUMBER: 09/216,021
R FILING DATE: December 16, 1998
R PAPLICATION NUMBER: 09/218,517
R FILING DATE: December 22, 1998
R APPLICATION NUMBER: 09/254,311
R FILING DATE: January 5, 1998
R APPLICATION NUMBER: 60/074,086
R FILING DATE: February 9, 1998
R APPLICATION NUMBER: 60/074,092
R FILING DATE: February 9, 1998
R APPLICATION NUMBER: 60/075,945
R FILING DATE: February 25, 1998
R APPLICATION NUMBER: 60/112,850
                                                                                                                                                              FILING DATE: December 16, 1998
APPLICATION NUMBER: 60/713, 296
FILING DATE: December 22, 1998
APPLICATION NUMBER: 60/346,222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: June 22,
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181 KVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPP 240
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                          241 TLLELHLDYNKISTVELEDFKRYKELQRLGIGNNKITDIENGSLANIPRVREIHLENNKL 300
                                                                                                           241 TLLELHLDYNKISTVELEDFKRYKELQRIGLGNNKITDIENGSLANIPRVREIHLENNKL 300
KVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPP 240
                        301 KKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQP 360
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100.0%; Pred. No. 2e-159;
tive 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/944,907
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PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 2:
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09944907
Publication No. US20020198147A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                     361 ATFRCVLSRMSVQLGNFGM 379
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Matches 379; Conservative
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APPLICANT: Botstein, David
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Roy, Margaret
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ORGANISM: Homo Sapien
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241 TLLELHLDYNKISTVELEDFKRYKELQRLGIGNNKITDIENGSLANIPRVREIHLENNKL 300
                      KKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQP 360
                                                                                  APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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CURRENT APPLICATION NUMBER: U5/09/944,929
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
                                                                                                                                                                                                                                           Sequence 2, Application US/09944929; Publication No. US20020197612A1
                                                                                                                                                                                                                                                                                                                                                                                                                               Grimaldi, Christopher
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Filvaroff, Ellen
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APPLICANT: Botstein, David
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Goddard, Audrey
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Hillan, Kenneth
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Matches 379; Conservative
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ORGANISM: Homo Sapien
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LENGTH: 379
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CURRENT APPLICATION NUMBER: US/10/028,072
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PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-08-26
PRIOR PLICATION NUMBER: 60/05974
PRIOR PLICATION NUMBER: 60/059113
PRIOR PLILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
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PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR PLING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06256
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06285
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06281
PRIOR FILING DATE: 1997-10-17
PRIOR PRILING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-24
                                                                                                                                                                                                                           Sequence 328, Application US/10028072 Publication No. US20030004311A1 GENERAL INFORMATION:
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FILING DATE: 1997-10-31
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                                                                  361 ATFRCVLSRMSVQLGNFGM 379
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Stewart, Timothy A.
Tumas, Daniel
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Gerritsen,Mary E.
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Wood, William
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Gurney, Austin L.
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Filvaroff, Ellen
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TITLE OF INVENTION:
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APPLICATION NUMBER: 60/063327

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063561

PRIOR PILING DATE: 1997-10-28

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PRIOR PILING DATE: 1997-10-28

PRIOR PILING DATE: 1997-10-29

PRIOR PILING DATE: 1997-11-27

PRIOR PILING DATE: 1997-11-17

PRIOR PILING DATE: 1997-11-17

PRIOR PILING DATE: 1997-11-12

PRIOR PILING DATE: 1997-12-16

PRIOR PILING DATE: 1998-01-29

PRIOR PILING DATE: 1998-01-29

PRIOR PILING DATE: 1998-01-29

PRIOR APPLICATION NUMBER: 60/07391

PRIOR PILING DATE: 1998-02-09

PRIOR PILING DATE: 1998-02-09

PRIOR PILING DATE: 1998-03-12

PRIOR PILING DATE: 1 R FILING DATE: 1997-10-27
R PAPLICATION NUMBER: 60/063329
R FILING DATE: 1997-10-27
R APPLICATION NUMBER: 60/063550
R FILING DATE: 1997-10-28
R FILING DATE: 1997-10-28
R FILING DATE: 1997-10-28 PRIOR PRIOR

PRIOR APPLICATION NUMBER: 60/08345
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-04-29
PRIOR PILING DATE: 1998-06-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR PILING DATE: 1998-05-07
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PRIOR PELING DATE: 1998-06-18
PRIOR PELING DATE: 1998-06-18
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PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-26
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Length 379; Indels

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100.0%; Score 1992; DB 9; ilarity 100.0%; Pred. No. 2e-159; Conservative 0; Mismatches 0;

Best Local Similarity Matches 379; Conserv

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                                                                                                                        181 KVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPP 240
                                                                                                                                          PRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEND 120
              FKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHEN 180
                                                                            241 TLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKL 300
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Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
Kljavin, Ivar
Napier, Mary
Roy, Margaret
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Filvaroff, Ellen
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APPLICANT: Botstein, David
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ORGANISM: Homo Sapien
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121 FKGLTSLYGLILINNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHEN 180
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                                                                      CURRENT APPLICATION NUMBER: US/09/944,449
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PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
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PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: December 16, 1997
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PRIOR FILLING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILLING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR PILLING DATE: December 18, 1997
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PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
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Patent No. US20020102647A1
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Filvaroff, Ellen
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APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548PIC1
CURRENT APPLICATION NUMBER: US/09/944,457
CURRENT FILING DATE: 2001-09-26
                                                       241 TLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKL 300
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PRIOR APPLICATION NUMBER: 09/866,028
PRIOR PILING DATE: 2001-09-26
PRIOR PLING DATE: 2001-05-25
PRIOR PLING DATE: D0-Cember 3, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR PILING DATE: December 11, 1997
PRIOR PILING DATE: December 12, 1997
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PRIOR APPLICATION NUMBER: 60/069,694
PRIOR PILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
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APPLICATION NUMBER: 60/070,440
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APPLICATION NUMBER: 60/074,092
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APPLICATION NUMBER: 60/075,945
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APPLICATION NUMBER: 60/074,
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APPLICANT: Botstein, David
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Hillan, Kenneth
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US-09-944-457-2
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APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US2002010264/Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
APPLICATION NUMBER: PCT/US99/28301
APPLICATION NUMBER: PCT/US99/28301
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                                                                                                              PRIOR PALLICATION NUMBER: 60/112,850
PRIOR PELING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR PLING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR PLING DATE: JULY 28, 1999
PRIOR PELING DATE: September 16, 1998
PRIOR PLING DATE: September 16, 1998
PRIOR PLING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR PLING DATE: December 16, 1998
PRIOR PLING DATE: December 16, 1998
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PRIOR PLING DATE: December 16, 1999
PRIOR PLING DATE: December 17, 1999
PRIOR PLING DATE: December 17, 1999
PRIOR PLING DATE: December 17, 1999
PRIOR PLING DATE: September 19, 1999
PRIOR PLING DATE: September 16, 1999
PRIOR PLING DATE: September 15, 1999
PRIOR PLING DATE: September 15, 1999
PRIOR PLING DATE: September 15, 1999
PRIOR PLING DATE: December 1, 1999
PRIOR PLING DATE: December 1, 1999
PRIOR PLING DATE: Pertury 2, 2000
PRIOR PLING DATE: Pertury 2, 2000
PRIOR PRIOR PELICATION NUMBER: PCT/US99/3095
PRIOR PLING DATE: February 11, 2000
PRIOR PRIOR PLING DATE: PERLURY 2, 2000
PRIOR PRIOR PLING DATE: PEDLURY 1, 2000
PRIOR PRIOR PRIOR DATE: PEDLURY 1, 2000
PRIOR PRIOR PRIING DATE: PEDLURY 1, 2000
PRIOR PRIOR PLING DATE: MATCH 3, 2000
PRIOR PRIOR PLING DATE: WAY 2, 2000
PRIOR PRIOR PLING DATE: PEDLURY 1, 2000
PRIOR PRIOR PLING DATE: DECEMBER: PCT/US00/20110
                                                                                           FILING DATE: February 25, 1998
APPLICATION NUMBER: 60/112,850
FILING DATE: December 16, 1998
APPLICATION NUMBER: 60/113,296
FILING DATE: December 22, 1998
            APPLICATION NUMBER: 60/074,092
FILING DATE: February 9, 1998
APPLICATION NUMBER: 60/075,945
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Best Local Similarity 100.0
Matches 379; Conservative
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ORGANISM: Homo Sapien
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CURRENT APPLICATION NUMBER: US/09/944,862
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: December 3, 1997
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PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR PLING DATE: December 11, 1997
PRIOR PELING DATE: December 11, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR PRILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
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APPLICATION NUMBER: 60/113,296
FILING DATE: December 22, 1998
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APPLICATION NUMBER: 60/069,873
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Filvaroff, Ellen
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APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US2002011085Alember 30, 1999
FILING DATE: No. US20020110859Alember 30, 1999
FILING DATE: No. US20020110859Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
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100.0%; Pred. No. 2e-159;
Live 0; Mismatches 0
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PRIOR APPLICATION NUMBER: 09/218, 517
PRIOR PILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254, 311
PRIOR FILING DATE: March 3, 1999
PRIOR PILING DATE: March 3, 1999
PRIOR FILING DATE: June 22, 1999
PRIOR PLING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
                                                                                                                                                     PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
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PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
                                                                                                            PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
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APPLICATION NUMBER: PCT/US00/03565
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APPLICATION NUMBER: PCT/US00/04414
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PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
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PRIOR FILING DATE: March 30, 2000
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PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
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PRIOR APPLICATION NUMBER: PCT/US00/32678
                   FILING DATE: December 16, 1998
APPLICATION NUMBER: 60/113,296
FILING DATE: December 22, 1998
APPLICATION NUMBER: 60/112,850
                                                                                         PRIOR APPLICATION NUMBER: 60/146,222
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Best Local Similarity 100.C
Matches 379; Conservative
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; ORGANISM: Homo Sapien
US-09-944-457-2
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LENGTH: 379
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241 TLLELHLDYNKISTVELEDFKRYKELQRLGGNNKITDIENGSLANIPRVREIHLENNKL 300
                                                              301 KKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQP 360
                                                                                                 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/945,587
CURRENT FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-05-25
301 KKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQP 360
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FILING DATE: July 28, 1999
APPLICATION NUMBER: PCT/US98/19330
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PRIOR FILING DATE: December 3, 1997
PRIOR PAPLICATION NUMBER: 60/069,334
PRIOR PELLING DATE: December 11, 1997
PRIOR PELLING DATE: December 11, 1997
PRIOR PAPLICATION NUMBER: 60/069,355
PRIOR FILING DATE: December 11, 1997
PRIOR PELLING DATE: December 11, 1997
PRIOR PELLING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR PELLING DATE: December 16, 1997
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PRIOR APPLICATION NUMBER: 60/069,696
PRIOR PELLING DATE: December 16, 1997
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APPLICATION NUMBER: 60/074,092
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APPLICATION UNDRER: 60/075,945
FILING DATE: February 25, 1998
APPLICATION NUMBER: 60/112,850
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                                                                                                                                                                                                                                                     Sequence 2, Application US/09945587; Patent No. US20020127643A1; GENERAL INFORMATION:
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Filvaroff, Ellen
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APPLICANT: Botstein, David
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Hillan, Kenneth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20020115145Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. US20020115145Alember 30, 1999
FILING DATE: December1, 1999
FILING DATE: December1, 1999
                                                                               PRIOR PILING DATE: September 16, 1998
PRIOR FILING DATE: September 16, 1998
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PRIOR PELING DATE: December 16, 1998
PRIOR PELING DATE: December 12, 1998
PRIOR PILING DATE: December 22, 1998
PRIOR PILING DATE: December 22, 1998
PRIOR PILING DATE: December 22, 1999
PRIOR PILING DATE: PECTUGS9/12552
PRIOR PILING DATE: June 22, 1999
PRIOR PILING DATE: June 22, 1999
PRIOR PILING DATE: December 15, 1999
PRIOR PILING DATE: POT 1999
PRIOR PILING DATE: December 15, 1999
PRIOR PILING DATE: December 16, 1999
PRIOR PILING DATE: PED PRIOR DECEMBER: PCT/US99/28301
PRIOR PILING DATE: PECTUGS9/28301
PRIOR PILING DATE: PECTUGS9/30055
PRIOR PELING DATE: PECTUGS9/30095
PRIOR PILING DATE: PED PRIOR POT/US00/04414
PRIOR PILING DATE: PED PRIOR POT/US00/0439
PRIOR PILING DATE: PED PRIOR POT/US00/08439
PRIOR PILING DATE: PED PRIOR POT/US00/08439
PRIOR PILING DATE: MATCH 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR PILING DATE: MATCH 30, 2000
PRIOR PILING DATE: DECEMBER: PCT/US00/32678
                                      FILING DATE: July 28, 1999
APPLICATION NUMBER: PCT/0598/19330
FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/0598/25108
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                 60/146,222
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           APPLICATION NUMBER:
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US-09-944-862-2
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APPLICATION NUMBER: PCT/US98/25108

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361 ATFRCVLSRMSVQLGNFGM 379

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APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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CURRENT APPLICATION NUMBER: US/09/945,015
CURRENT FILING DATE: 2001-09-26
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PRIOR APPLICATION NUMBER: PCT/US98/25108
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PRIOR APPLICATION NUMBER: 09/866,028

PRIOR FILING DATE: 2001-09-26

PRIOR PELING DATE: 2001-05-26

PRIOR PELING DATE: DECEMBER 3, 1997

PRIOR PELING DATE: DECEMBER 1, 1997

PRIOR FILING DATE: DECEMBER 11, 1997

PRIOR FILING DATE: DECEMBER 11, 1997

PRIOR APPLICATION NUMBER: 60/069,334

PRIOR PELING DATE: DECEMBER 11, 1997

PRIOR APPLICATION NUMBER: 60/069,425

PRIOR PELING DATE: DECEMBER 12, 1997

PRIOR APPLICATION NUMBER: 60/069,696

PRIOR PELING DATE: DECEMBER 16, 1997

PRIOR APPLICATION NUMBER: 60/069,696

PRIOR PELING DATE: DECEMBER 16, 1997

PRIOR APPLICATION NUMBER: 60/069,870

PRIOR APPLICATION NUMBER: 60/069,870

PRIOR PELING DATE: DECEMBER 16, 1997

PRIOR PELING DATE: DECEMBER 17, 1997

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APPLICATION NUMBER: 60/068,017
FILING DATE: December 18, 1997
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PRIOR FILING DATE: January 5, 1998
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APPLICATION NUMBER: 60/074,086
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PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
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PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
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                                                                                                           Sequence 2, Application US/09945015 Patent No. US20020132768A1
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Grimaldi,Christopher
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APPLICANT: Botstein, David
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Kljavin, Ivar
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Tumas, Daniel
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Ouery Match 100.0%; Score 1992; DB 10
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 379; Conservative 0; Mismatches 0;
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PRIOR FILING DATE: February 11, 2000
PRIOR FILING DATE: February 22, 2000
PRIOR FILING DATE: February 22, 2000
PRIOR PELING DATE: March 2, 2000
PRIOR PELING DATE: March 2, 2000
PRIOR PELING DATE: March 3, 2000
PRIOR PELING DATE: March 30, 2000
PRIOR FILING DATE: May 22, 2000
PRIOR FILING DATE: May 22, 2000
PRIOR FILING DATE: May 22, 2000
PRIOR FILING DATE: JULY 28, 2000
PRIOR FILING DATE: JULY 28, 2000
PRIOR PRIOR CATION NUMBER: PCT/USO0/20710
PRIOR PRIOR DATE: JULY 28, 2000
PRIOR APPLICATION NUMBER: PCT/USO0/30678
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PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
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US-09-945-587-2
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LENGIH: 379
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APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE KEEKEKEN JON NUMBER: US/09/944,396
CURRENT FILING DATE: 2001-09-26
PRIOR PAPLICATION NUMBER: 09/866,028
PRIOR PAPLICATION NUMBER: 60/067,411
PRIOR PILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR PILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 11, 1997
PRIOR PILING DATE: December 16, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR PRILING DATE: December 17, 1997
PRIOR PRILING DATE: December 17, 1997
PRIOR PILING DATE: December 17, 1997
PRIOR FILING DATE: PEDIUARY 9, 1998
PRIOR FILING DATE: PEDIUARY 9, 1998
PRIOR FILING DATE: FEDIUARY 9, 1998
PRIOR FILING DATE: FEDIUARY 9, 1998
PRIOR FILING DATE: PEDIUARY 25, 1998
PRIOR FILING DATE: PEDCUARY 9, 1998
PRIOR FILING DATE: PEDCUARY 9, 1998
PRIOR FILING DATE: PEDCUARY 9, 1999
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 11, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: SEPTEMBER: 60/2146, 222
PRIOR PRILOR DATE: December 16, 1998
PRIOR FILING DATE: SEPTEMBER: 09/218, 517
PRIOR PRILOR DATE: December 16, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR PILING DATE: DECEMBER: 09/218, 517
PRI
               Sequence 2, Application US/09944396 Patent No. US20020132981A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                     Godowski,Paul
Grimaldi,Christopher
                                                                                                                                                                                               Filvaroff, Ellen
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Kljavin, Ivar
                                                                                                             APPLICANT: Baker, Kevin APPLICANT: Botstein, David
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Tumas, Daniel
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                                                   PRIOR APPLICATION NUMBER: 09/254,311
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR FILING DATE: June 22, 1999
PRIOR FILING DATE: September 15, 1999
PRIOR FILING DATE: September 15, 1999
PRIOR FILING DATE: No. US2002013768Alember 30, 1999
PRIOR FILING DATE: No. US2002013768Alember 30, 1999
PRIOR FILING DATE: No. US2002013768Alember 30, 1999
PRIOR PRILING DATE: No. US2002013768Alember 30, 1999
PRIOR FILING DATE: December1, 1999
PRIOR FILING DATE: December1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/3005
PRIOR PRILING DATE: December 16, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR PRILING DATE: December 16, 1999
PRIOR PRILING DATE: PORTURY 11, 2000
PRIOR APPLICATION NUMBER: PCT/US09/0365
PRIOR PRILICATION NUMBER: PCT/US09/0365
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PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR FILING DATE: MARCH 2, 2000
PRIOR APPLICATION NUMBER: PCT/USO0/08439
PRIOR APPLICATION NUMBER: PCT/USO0/14042
PRIOR FILING DATE: MAY 22, 2000
PRIOR FILING DATE: MAY 22, 2000
PRIOR FILING DATE: JUJY 28, 2000
PRIOR FILING DATE: JUJY 28, 2000
PRIOR FILING DATE: JUJY 28, 2000
PRIOR PLILNG DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/USO0/32678
PRIOR FILING DATE: DECEMBER 1, 2000
PRIOR PRIOR DATE: PEDRUARY 28, 2001
APPLICATION NUMBER: 09/218,517 FILING DATE: December 22, 1998 APPLICATION NUMBER: 09/254,311
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US-09-945-015-2
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RESULT 14

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Botstein, David
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Hillan, Kenneth
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                                                                                            PRIOR FILING DATE: NO. US20020132981Alember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: NO. US20020132981Alember 30, 1999
PRIOR FILING DATE: NO. US20020132981Alember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December1, 1999
                                                                                                                                                                                                                                      PRIOR PAPLICATION NUMBER: PCT/USO0/03565
PRIOR FLING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR APPLICATION NUMBER: PCT/USO0/05841
PRIOR PELING DATE: March 2, 2000
PRIOR PELING DATE: March 3, 2000
PRIOR PELING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/USO0/14042
PRIOR PLING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/USO0/14042
PRIOR APPLICATION NUMBER: PCT/USO0/14042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/USO0/20/110
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
LENGTH: 379
                 PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
                                                                                                                                                                                FILING DATE: December1, 1999
APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/12252
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US-09-944-396-2
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Best Local Similarity
Matches 379; Conserv
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US-09-944-097-2
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME PLICE PEASUBLY CURRENT ACIDS ENCODING THE SAME PLICE REFERENCE: P25.4991C1 CURRENT APPLICATION NUMBER: U5/09/944,097 CURRENT FILING DATE: 2001-08-31 PRIOR APPLICATION NUMBER: 09/866,028 PRIOR APPLICATION NUMBER: 09/069,334 PRIOR FILING DATE: December 11, 1997 PRIOR FILING DATE: December 11, 1997 PRIOR FILING DATE: December: 11, 1997 PRIOR FILING DATE: December: 00/069,278 PRIOR FILING DATE: December: 00/069,278
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PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020133675Alember 30, 1999
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PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR PRIOR DATE: December 16, 1998
PRIOR PRIOR DATE: December 16, 1998
PRIOR PELING DATE: December 22, 1998
PRIOR PELING DATE: December 22, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR PELING DATE: MATCH 3, 1999
PRIOR PLING DATE: MATCH 3, 1999
PRIOR APPLICATION NUMBER: 09/254, 311
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PRIOR APPLICATION NUMBER: PCT/US99/21090
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PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR FILING DATE: December 18, 1997
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PRIOR APPLICATION NUMBER: 60/070,440
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PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
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PRIOR APPLICATION NUMBER: 60/069,696
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PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: Pebruary 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
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FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,870
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Ferrara, Napoleone
Filvaroff, Ellen
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/06/334
PRIOR FILING DATE: December 11, 1997
PRIOR PAPLICATION NUMBER: 60/06/335
PRIOR PAPLICATION NUMBER: 60/06/335
PRIOR PILING DATE: December 11, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR PELING DATE: December 17, 1997
PRIOR PELING DATE: PEDIUARY 5, 1998
PRIOR FILING DATE: PEDIUARY 9, 1998
PRIOR FILING DATE: PEDIUARY 9, 1998
PRIOR FILING DATE: PEDIUARY 25, 1998
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PRIOR FILING DATE: PEDEUARY 25, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: SEPTEMBER: 60/146, 221
PRIOR PELICATION NUMBER: 60/218, 2199
PRIOR FILING DATE: December 16, 1998
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FILING DATE: September 15, 1999
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APPLICATION NUMBER: PCT/US99/28409
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PRIOR APPLICATION NUMBER: PCT/US99,
PRIOR FILING DATE: December1, 1999
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Grimaldi, Christopher
Gurney, Austin
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Goddard, Audrey
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                                                                                                                                                                                                   Roy, Margaret
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                                 PRIOR FILING DATE: No. US20020133675Alember 30, 1999 PRIOR APPLICATION NUMBER: PCT/US99/28301
                                                                               PRIOR APPLICATION NUMBER: PC1/039/2001
PRIOR APPLICATION NUMBER: PC1/039/2009
PRIOR FILING DATE: December1 16, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR PELING DATE: POFT/0500/03565
PRIOR PELING DATE: February 11, 2000
PRIOR FILING DATE: February 22, 2000
PRIOR FILING DATE: February 22, 2000
PRIOR FILING DATE: March 2, 2000
PRIOR PLICATION NUMBER: PCT/0500/08419
PRIOR PLILING DATE: March 30, 2000
PRIOR PLING DATE: MAY 22, 2000
PRIOR PLING DATE: MAY 22, 2000
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PRIOR FILING DATE: DECEMBER: PCT/0500/20710
PRIOR PELICATION NUMBER: PCT/0500/20710
PRIOR PELING DATE: DECEMBER: DCT/0500/20710
PRIOR PELING DATE: PEDELOGATION NUMBER: PCT/0500/20710
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Patent No. US20020142419A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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                                                                                                              PRIOR AFFLICATION NUMBER: PCT/NGU/03565
PRIOR FLING DATE: February 11, 2000
PRIOR FLING DATE: February 21, 2000
PRIOR PLING DATE: February 22, 2000
PRIOR PELING DATE: February 22, 2000
PRIOR PELING DATE: March 2, 2000
PRIOR PELING DATE: March 30, 2000
PRIOR PELING DATE: March 30, 2000
PRIOR PELING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/USO0/14042
PRIOR PLING DATE: May 22, 2000
PRIOR PLING DATE: July 28, 2000
PRIOR PLING DATE: December 1, 2000
PRIOR PLING DATE: December 1, 2000
PRIOR PLING DATE: PEDT/USO1/06520
                                   PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCI/US00/03565
APPLICATION NUMBER: PCT/US99/30095
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Patent No. US20020142958A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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Filvaroff, Ellen
Gerritsen, Mary
Goddarr, Audrey
Godowski, Paul
Grimaldi, Christopher
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Best Local Similarity 100.0
Matches 379; Conservative
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ORGANISM: Homo Sapien
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TITLE OF INVENTION: SECRETED AND TRANSMENBERANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILLE PEFERENCE: P2548PICI
CURRENT APPLICATION NUMBER: US/09/943,762
PRIOR APPLICATION NUMBER: US/086,028
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: December 16, 1997
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PRIOR PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR PRIOR DATE: December 16, 1997
PRIOR PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
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PRIOR FILING DATE: No. US20020142958Alember 30, 1999
PRIOR PELLING DATE: DCT/US99/28301
PRIOR FILING DATE: December1, 1999
PRIOR PLILNG DATE: December1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
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PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: NO. US20020142958Alem
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FILING DATE: June 22, 1999
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APPLICATION NUMBER: PCT/US00/03565
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R FILING DATE: December 16, 1998
R APPLICATION NUMBER: 09/218,517
R FILING DATE: December 22, 1998
R APPLICATION NUMBER: 09/254,311
R FILING DATE: March 3, 1999
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PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR PLICATION NUMBER: 60/068,017
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FILING DATE: December 18, 1997
APPLICATION NUMBER: 60/070,440
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APPLICATION WIMBER: 60/074, 086
ALLING DATE: FEDRUARY 9, 1998
APPLICATION NUMBER: 60/074,092
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APPLICATION NUMBER: 60/113,296
FILING DATE: December 22, 1998
PELING DATE: July 28, 1999
FILING DATE: July 28, 1999
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FILING DATE: February 25, 1998
APPLICATION NUMBER: 60/112,850
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PRIOR FILING DATE: February 11, 2000
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Napier, Mary
Roy, Margaret
                                                                                                                  Wood, William
                                                                                 Tumas, Daniel
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC FILLE WOOD, WILliam TITLE OF INVENTION: ACIDS ENCODING THE SAME FILLE PARKET FILLE OF INVENTION: ACIDS ENCODING THE SAME FILLE FILLE PARKET PAPLICATION NUMBER: US/09/944,654

CURRENT FILLNG DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 09/866,028

PRIOR PILLING DATE: December 3, 1997

PRIOR PILLING DATE: December 11, 1997

PRIOR PILLING DATE: December 12, 1997

PRIOR PILLING DATE: December 12, 1997

PRIOR PILLING DATE: December 16, 1997

PRIOR PILLING DATE: December 16, 1997

PRIOR PILLING DATE: December 16, 1997

PRIOR PLICATION NUMBER: 60/069,694

PRIOR PLICATION NUMBER: 60/069,917

PRIOR PLICATION NUMBER: 60/074,098

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PRIOR PLICATION NUMBER: 60/074,098

PRIOR PLICATION NUMBER: 60/075,945

PRIOR PLICATION NUMBER: 60/075,945

PRIOR PLICATION NUMBER: 60/075,945

PRIOR PLICATION NUMBER: 60/0712,850

PRIOR APPLICATION NUMBER: 60/0713,296

PRIOR APPLICATION NUMBER: 60/0713,296

PRIOR PRIOR DATE: December 16, 1997

PRIOR PLICATION NUMBER: 60/0713,296

PRIOR PRIOR DATE: December 16, 1997

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PRIOR PRIOR DATE: December 16, 1998

PRIOR PLICATION NUMBER: 60/0713,296
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OR APPLICATION NUMBER: 60/04,086
OR PELLING DATE: February 9, 1998
OR APPLICATION NUMBER: 60/074,092
OR FILING DATE: February 9, 1998
OR FILING DATE: February 9, 1998
OR PILING DATE: February 25, 1998
OR APPLICATION NUMBER: 60/112,850
OR PILING DATE: December 16, 1998
OR APPLICATION NUMBER: 60/113,296
OR FILING DATE: December 22, 1998
OR FILING DATE: December 22, 1998
OR FILING DATE: 04046,222
OR FILING DATE: 04046,222
OR FILING DATE: 0414,28, 1999
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APPLICATION NUMBER: PCT/USO0/O4414
FILING DATE: February 22, 2000
APPLICATION NUMBER: PCT/USO0/05841
FILING DATE: MARCH 2, 2000
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APPLICATION NUMBER: PCT/US99/12252
TITING DATE: June 22, 1999
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APPLICATION NUMBER: PCT/US99/28409
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APPLICATION NUMBER: PCT/US00/03565
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APPLICATION NUMBER: PCT/US98/25108
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APPLICATION NUMBER: 09/218,517
FILING DATE: December 22, 1998
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APPLICATION NUMBER: 09/216,021
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       Tumas, Daniel
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PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR PLING DATE: May 22, 2000
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: July 28, 2000
PRIOR PILING DATE: July 28, 2000
PRIOR FILING DATE: July 28, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 2: SEQ ID NOS: 120
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Grimaldi, Christopher
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Filvaroff, Ellen
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Goddard, Audrey
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Kljavin, Ivar
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APPLICANT: Botstein, David
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Roy, Margaret
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US-09-943-762-2
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US-09-944-654-2
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PRIOR FILING DATE: December 11
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          FILE REFERENCE: P2548P1C1
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PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR PLING DATE: MAY 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR PFILING DATE: July 28, 2000
PRIOR PFLING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR PLILING DATE: PEDRUARY PCT/US01/06520
PRIOR PLILING DATE: FEBRUARY 28, 2001
NUMBER OF SEQ ID NOS: 120
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Patent No. US20020150976A1
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Grimaldi, Christopher
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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Hillan, Kenneth
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US-09-944-654-2
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LENGTH: 379
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FILING DATE: September 15, 1999
APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20020150976Alember 30, 1999
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FILING DATE: No. US20020150976Alember 30, 1999
CURRENT APPLICATION NUMBER: US/09/943,851A CURRENT FILING DATE: 2001-08-30
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RAPLICATION NUMBER: 60/13, 296

PR FILING DATE: December 22, 1998

PR APPLICATION NUMBER: 60/146,222

PR FILING DATE: 38, 1999

RAPLICATION NUMBER: PCT/059/19330

PRILING DATE: September 16, 1998
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APPLICATION NUMBER: PCT/US99/21090
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FILING DAPER: MATCH 30, 2000
APPLICATION NUMBER: PCT/US00/14042
FILING DATE: May 22, 2000
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PRIOR FILING DATE: December 16, 1999
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PRIOR APPLICATION NUMBER: PCT/USO0/03565
                                     CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: US/09/866,028
PRIOR FILING DATE: 2001-05-25
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PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR FILING DATE: February 9, 1998
PRIOR FILING DATE: February 25, 1998
PRIOR FILING DATE: February 25, 1998
PRIOR PLING DATE: February 25, 1998
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PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
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PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR PELING DATE: December 17, 1997
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
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PRIOR APPLICATION UNBER: 60/06335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
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APPLICATION NUMBER: 60/070,440
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APPLICATION WUMBER: 09/216, 021
ELING DATE: December 16, 1998
APPLICATION NUMBER: 09/218,517
                                                                                                                                 PRIOR APPLICATION NUMBER: 60/067,411
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PRIOR APPLICATION NUMBER: 60/069,334
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FILING DATE: March 3, 1999
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100.0%; Pred. No. 2e-159;
tive 0; Mismatches 0
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: PCT/US00/20710 PRIOR FILING DATE: July 28, 2000 PRIOR PLICATION NUMBER: PCT/US00/32678 PRIOR FILING DATE: December 1, 2000 PRIOR PLICATION NUMBER: PCT/US01/06520 PRIOR FILING DATE: February 28, 2001 NUMBER OF SEQ ID NOS: 120
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Patent No. US20020052308A1
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SOFTWARE: PatentIn Ver. 2.0
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US-09-925-301-1561
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LENGTH: 155
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                                                                                                                                                  LENGTH: 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 KGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIE-NGSLANIPRVREIH 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 LENNKLKKIPSGLPELK--YLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNP 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSYNKLKNIPTVNENLENYYLEV-----NQLEKFDIKSFCKILGPLSYSKIKHLRLDGNR 330
                                                                                                                                                                                                                         177 IHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVP 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 NDFKGLTSLYGLILNNNKL--TKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELR 176
                                                                                                                    176 RIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSV 234
                                                                                                                                                                                                  235 PKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIH 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 FPFDLF----PMCPFGCQC---YSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKE 118
                                                                                                                                           Gaps
                                                                              Gaps
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                                      Length 155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70; Mismatches 128; Indels
                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al. IIILE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                   20.4%; Score 406.5; DB 10; 50.3%; Pred. No. 3.3e-27;
                                                                            42;
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                                                                            33; Mismatches
                                                                                                                                                                                                                                                                                                       295 LENNKLKKIPSGLPELKYLQIIFLHSNSIARVG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/USO0/05882
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 980, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
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                                                                            77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 102; Conserva
                                                         Best Local Similarity
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LOCATION: (333)
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US-09-925-301-1561
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TYPE: PRT
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353 VKYWEMQPATFRCVLSRMSVQL 374

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

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CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-25
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/059113 PRIOR APPLICATION NUMBER: 60/059117
PRIOR PILING DATE: 1997-09-17
PRIOR PLILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PLILING DATE: 1997-09-17
PRIOR PLILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR PLILING DATE: 1997-09-18
PRIOR PLILOATION NUMBER: 60/059352
PRIOR PLILOATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19 PRIOR APPLICATION NUMBER: 60/062285
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06287
PRIOR FILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/062814
PRIOR APPLICATION NUMBER: 60/062814 Sequence 302, Application US/10028072 Publication No. US20030004311A1 GENERAL INFORMATION: APPLICANT: Baker Kevin P. APPLICANT: Beresini, Maureen PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059836
PRIOR FILING DATE: 1997-09-24
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17 APPLICATION NUMBER: 60/063045 FILING DATE: 1997-10-24 APPLICATION NUMBER: 60/063082 PRIOR APPLICATION NUMBER: 60/059115 PRIOR FILING DATE: 1997-09-17 APPLICATION NUMBER: 60/062816 FILING DATE: 1997-10-24 APPLICATION NUMBER: 60/063127 FILING DATE: 1997-10-24 APPLICATION NUMBER: 60/063327 FILING DATE: 1997-10-27 Desnoyers, Luc Filvaroff, Ellen Gao, Wei-Qiang Gerritsen, Mary E. Goddard, Audrey Stewart, Timothy A. Watanabe, Colin K Wood, William FILING DATE: 1997-10-31 Godowski, Paul J. Gurney, Austin L. Sherwood, Steven Smith, Victoria DeForge, Laura Tumas,Daniel APPLICANT: Zhang TITLE OF INVENTION: FILE REFERENCE: us-10-028-072-302 APPLICANT: RESULT 22 PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR

APPLICATION NUMBER: 60/063329 FILING DATE: 1997-10-27 APPLICATION NUMBER: 60/063550

PRIOR

R APPLICATION NUMBER: 60/074086
R FILING DATE: 1998-02-09
R APPLICATION NUMBER: 60/074092
R FILING DATE: 1998-02-09
R APPLICATION NUMBER: 60/077791
R FILING DATE: 1998-03-12 FILING DATE: 1997-10-28 APPLICATION NUMBER: 60/063704 FILING DATE: 1997-10-29 FILING DATE: 1997-10-28 APPLICATION NUMBER: 60/063561 FILING DATE: 1997-10-29 APPLICATION NUMBER: 60/063733 APPLICATION NUMBER: 60/063735 APPLICATION NUMBER: 60/063738 APPLICATION NUMBER: 60/064248 FILING DATE: 1997-11-03 APPLICATION NUMBER: 60/064809 APPLICATION NUMBER: 60/065186 FILING DATE: 1997-11-12 APPLICATION NUMBER: 60/065846 FILING DATE: 1997-11-17 APPLICATION NUMBER: 60/066770 FILING DATE: 1997-11-24 APPLICATION NUMBER: 60/072320 FILING DATE: 1998-01-23 APPLICATION NUMBER: 60/073612 PRIOR APPLICATION NUMBER: 60/083322 PRIOR FILING DATE: 1998-04-28 PRIOR PPLICATION NUMBER: 60/083545 PRIOR FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/063755 APPLICATION NUMBER: 60/066453 FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/066511 APPLICATION NUMBER: 60/069212 FILING DATE: 1997-12-11 APPLICATION NUMBER: 60/069694 APPLICATION NUMBER: 60/078910 APPLICATION NUMBER: 60/079728 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/081203 FILING DATE: 1998-04-09 PRIOR FILLING DATE: 1998-04-15 PRIOR APPLICATION NUMBER: 60/082999 APPLICATION NUMBER: 60/066364 60/069278 APPLICATION NUMBER: 60/069334 FILING DATE: 1998-03-25 APPLICATION NUMBER: 60/079663 APPLICATION NUMBER: 60/080165 FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/081229 APPLICATION NUMBER: 60/079294 APPLICATION NUMBER: 60/081695 PRIOR APPLICATION NUMBER: 60/081817 APPLICATION NUMBER: 60/081818 FILING DATE: 1997-10-29 FILING DATE: 1997-10-29 FILING DATE: 1998-04-14 1997-10-29 FILING DATE: 1997-11-07 FILING DATE: 1997-12-16 FILING DATE: 1998-03-20 FILING DATE: 1998-02-27 FILING DATE: 1998-04-09 1998-04-15 FILING DATE: 1998-04-24 FILING DATE: 1997-11-24 FILING DATE: 1998-02-04 FILING DATE: 1997-10-1 FILING DATE: 1997-11-21 FILING DATE: 1998-03-31 FILING DATE: 1997-12-1; 1997-12-1 APPLICATION NUMBER: FILING DATE: FILING DATE: FILING DATE: PRIOR PRIOR

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APPLICANT:
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APPLICANT:
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PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
PRIOR PAPLICATION NUMBER: 60/084637
PRIOR PLING DATE: 1998-05-07
PRIOR PAPLICATION NUMBER: 60/085149
PRIOR PELING DATE: 1998-05-13
PRIOR PAPLICATION NUMBER: 60/085338
PRIOR PELING DATE: 1998-05-13
PRIOR PAPLICATION NUMBER: 60/085339
PRIOR PELING DATE: 1998-05-13
PRIOR PAPLICATION NUMBER: 60/085579
PRIOR PELING DATE: 1998-05-13
PRIOR PELING DATE: 1998-05-13
PRIOR PELING DATE: 1998-05-13
PRIOR PELING DATE: 1998-05-13
PRIOR PELING DATE: 1998-05-15
PRIOR PELING DATE: 1998-05-16
PRIOR PELING DATE: 1998-05-17
PRIOR PELING DATE: 1998-05-18
PRIOR PELING DATE: 1998-05-19
PRIOR PELING DATE: 1998-06-10
PRIOR PELING DATE: 1998-06-13
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-27
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Best Local Similarity
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267 NKLQDIPY-NIFNLPNIVELSVGHNKLKQAFYIPRNLEHL-----YLQNNEIEKMNLTV 319
                                                                                                                       207 IFAKMEKLMQLNLCSNRLESMPPGLPSSLMYLSLENNSISSIPEKYFDKLPKLHTLRMSH 266
155 YLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPG 214
                                                                                                                                                                                           274 NKITDIENGSLANIPRVREIHLENNKLKK---IPSGLPELKYLQIIFLHSNSIARVGVND 330
                                                                                             215 AFEGV-TVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
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PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR PELING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-17
PRIOR FILING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR PELING DATE: 1997-09-18
PRIOR PELING DATE: 1997-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 36, Application US/10028072 Publication No. US20030004311A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1997-09-19
APPLICATION UNBABER: 60/059588
FILING DATE: 1997-09-19
APPLICATION NUMBER: 60/059836
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                                                                                                                                                                                                                                                                                           331 FCPTVPKMKKSLYSAISLFNNPVK 354
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Stewart, Timothy A
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Watanabe, Colin K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maureen
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Filvaroff, Ellen
Gao, Wei-Qiang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang
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R APPLICATION NUMBER: 60/063735

R FILING DATE: 1997-10-29

R APPLICATION NUMBER: 60/063738

R FILING DATE: 1997-10-29

R APPLICATION NUMBER: 60/063755

R APPLICATION NUMBER: 60/064248

R FILING DATE: 1997-11-07

R APPLICATION NUMBER: 60/064809

R FILING DATE: 1997-11-10

R APPLICATION NUMBER: 60/065186

R FILING DATE: 1997-11-12

R APPLICATION NUMBER: 60/065846

R FILING DATE: 1997-11-24

R APPLICATION NUMBER: 60/066364

R FILING DATE: 1997-11-24

R APPLICATION NUMBER: 60/066453

R FILING DATE: 1997-11-24

R APPLICATION NUMBER: 60/066511

R APPLICATION NUMBER: 60/066511

R APPLICATION NUMBER: 60/066511

R FILING DATE: 1997-11-24

R APPLICATION NUMBER: 60/066511

R FILING DATE: 1997-11-24

R APPLICATION NUMBER: 60/066770

R APPLICATION NUMBER: 60/066710

R APPLICATION NUMBER: 60/066712

R APPLICATION NUMBER: 60/066712 R FILING DATE: 1997-10-24

R APPLICATION NUMBER: 60/063045

R FILING DATE: 1997-10-24

R APPLICATION NUMBER: 60/063082

R FILING DATE: 1997-10-31

R APPLICATION NUMBER: 60/063127

R APPLICATION NUMBER: 60/063127

R APPLICATION NUMBER: 60/063127 DR APPLICATION NUMBER: 60/063327

DR FILING DATE: 1997-10-27

DR APPLICATION NUMBER: 60/063329

DR FILING DATE: 1997-10-27

DR APPLICATION NUMBER: 60/063550

DR FILING DATE: 1997-10-28 R APPLICATION NUMBER: 60/063561 R FILING DATE: 1997-10-28 R APPLICATION NUMBER: 60/063704 R FILING DATE: 1997-10-29 R APPLICATION NUMBER: 60/063733 R FILING DATE: 1997-10-29 R FILING DATE: 1997-12-16

R APPLICATION NUMBER: 60/072320

R APPLICATION NUMBER: 60/073612

R APPLICATION NUMBER: 60/074086

R FILING DATE: 1998-02-04

R FILING DATE: 1998-02-09

R FILING DATE: 1998-02-09 APPLICALLO.
FILING DATE: 1998-03-51
APPLICATION NUMBER: 60/081203 APPLICATION NUMBER: 60/069278 FILLING DATE: 1997-12-11 APPLICATION NUMBER: 60/069334 FILLING DATE: 1997-12-11 APPLICATION NUMBER: 60/069694 APPLICATION NUMBER: 60/078910 FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/079294 APPLICATION NUMBER: 60/077791 FILING DATE: 1998-03-12 APPLICATION NUMBER: 60/079728 APPLICATION NUMBER: 60/081229 1998-02-09 1998-03-25 1998-02-27 FILING DATE: 1998-03 APPLICATION NUMBER: FILING DATE: 1998-02 FILING DATE: PRILOR RELATIONS PRILOR PRIOR

PRIOR APPLICATION NUMBER: 06/081695
PRIOR PILING DATE: 1998-04.14
PRIOR PILING DATE: 1998-04.15
PRIOR PELING DATE: 1998-04.25
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PRIOR PELING DATE: 1998-05.07
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PRIOR PELING DATE: 1998-05.15
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PRIOR PELING DATE: 1998-05.18
PRIOR PELING DATE: 1998-05.18
PRIOR PELING DATE: 1998-06.10
PRIOR PELING DATE: 1998-06.13
PRIOR PELING DATE: 1998-06.23

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                                                                                                                                                    74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 NALHVLEMSANPLDNNGIEPGAF-EGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKI 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253 STVELEDFKRYKELQRLGLGNNKITD--IENGSLANIPRVREIHLENNKLKKIPSGLPEL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
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                                                                                            Gaps
                                                                                                                                                                                                     134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGM 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INFORMATION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT214
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 646
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Best Local Similarity 33.0%; Pred. No. 3.9e-20;
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Patent No. US20020042386A1
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                                                                            92; Conservative
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                                            Best Local Similarity
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LENGTH: 623
    Query Match
                                                                                Matches
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APPLICANT: Eaton, Dan L.

APPLICANT: Eaton, Dan L.

APPLICANT: Gerritaen, Mary E.

APPLICANT: Godowski, Paul J.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Wood, William I.

APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3230R1C1

CURRENT APPLICATION NUMBER: US/10/063,547

CURRENT FILING DATE: 2002-05-02

PRIOT APPLICATION FILING PAGE: 2002-05-02

NUMBER OF SEQ ID NOS: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 STISSPSLOGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGT 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/10004551
Publication No. US20030004310A1
GENERAL INFORMATION:
APPLICANT: SHIMKETS, RICHARD A
APPLICANT: FERNANDES, ELMA
TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES ENCODED THEREBY
FILLE REFREENCE: 15966-559
CURRENT APPLICATION NUMBER: US/10/004,551
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 09/635,949
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 110
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 649;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.6%; Score 331.5; DB 9; Length (33.0%; Pred. No. 4.1e-20;
Live 37; Mismatches 111; Indels
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No. US20020182638A1
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Best Local Similarity 33.09
Matches 86; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo Sapien
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Best Local Similarity
                         GENERAL INFORMATION
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US-10-004-551-6
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LENGTH: 649
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248 N-LRKLYLQDNHINRVPPNAF 267

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CURRENT APPLICATION NUMBER: US/10/174,590
CURRENT FILING DATE: 2002-06-18
Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 384
LENGTH: 649
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                                                                                           134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGM 193
                                                                                                                        72 NAGI----PSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRTITYDSLSKI 127
                                                                                                                                                                                        194 NALHVLEMSANPLDNNGIEPGAFEGVTVFHIR-IAEAKLTSVPKGLPPTLLELHLDYNKI 252
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APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
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APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
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APPLICANT:
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APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C104
CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT FILING DATE: 2002-06-21
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Best Local Similarity 33.0%; Pred. No. 4.1e-20;
Matches 86; Conservative 37; Mismatches 111;
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                 ; Sequence 384, Application US/10176758 ; Publication No. US20030008353Al ; GENERAL INFORMATION:
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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
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APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
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Godowski, Paul J.
Gurney, Austin L.
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                                                                                                                                            Desnoyers, Luc
                                                                                              APPLICANT: Baker, Kevin P.
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US-10-176-758-384
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LENGTH: 649
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C50
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                                                                                                                                                                                DB 9; Length 649;
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CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,616
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
                                                                                                                                                                              16.6%; Score 331.5; DB 9; 33.0%; Pred. No. 4.1e-20; tive 37; Mismatches 111;
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Publication No. US20030013153A1
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Wood, William I.
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Godowski, Paul J.
Gurney, Austin L.
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US-10-063-616-132
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                                                                              SEQ ID NO 132
LENGTH: 649
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APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                                                                                                                                                                                                                                                                                                                                        194 NALHVLEMSANPLDNNGIEPGAFEGVTVFHIR-IAEAKLTSVPKGLPPTLLELHLDYNKI 252
                                                                                                                                                                                                                  134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGM 193
                                                    TITLE OF INVENTION: ACLIDS ENCODING THE STATE CURRENT APPLICATION NUMBER: US/10/006,867 CURRENT APPLICATION NUMBER: US/10/006,867 CURRENT FILMG DATE: 2001-12-06 PRIOR PEPLICATION NUMBER: 60/064215 PRIOR PELLING DATE: 1997-10-29 PRIOR PELLING DATE: 1997-10-29 PRIOR PELLING DATE: 1998-04-22 PRIOR FILLING DATE: 1998-04-22 PRIOR PELLING DATE: 1998-04-29 PRIOR PELLING DATE: 1998-04-29 PRIOR PELLING DATE: 1998-04-29 PRIOR PELLING DATE: 1998-04-29 PRIOR PELLING DATE: 1998-05-15 PRIOR PELLING DATE: 1998-05-05 PRIOR PELLING DATE: 1998-05-07 PRIOR PELLING DATE: 1998-05-07 PRIOR PELLING DATE: 1998-05-07 PRIOR PELLING DATE: 1998-06-07 PRIOR PELLING DATE: 
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APPLICATION NUMBER: 60/089105
APPLICATION NUMBER: 60/089514
APPLICATION NUMBER: 60/089514
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088740
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APPLICATION NUMBER: 60/088863
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APPLICATION NUMBER: 60/089653
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APPLICATION NUMBER: 60/088030
FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088811
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APPLICATION NUMBER: 60/088825
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Grimaldi, Christopher J.
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Watanabe, Colin K.
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US-10-006-867-132
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R APPLICATION NUMBER: 60/099741

R APPLICATION NUMBER: 60/099763

RR APPLICATION NUMBER: 60/099792

RR FILING DATE: 1998-09-10

RR APPLICATION NUMBER: 60/099912

RR FILING DATE: 1998-09-10

RR APPLICATION NUMBER: 60/099812

RR APPLICATION NUMBER: 60/099815

RR APPLICATION NUMBER: 60/10

RR APPLICATION NUMBER: 60/10627

RR APPLICATION NUMBER: 60/10627 R FILING DATE: 1998-08-18
R APPLICATION NUMBER: 60/096959
R FILING DATE: 1998-08-18
APPLICATION NUMBER: 60/097954
R FILING DATE: 1998-08-26
R APPLICATION NUMBER: 60/097971 DR APPLICATION NUMBER: 60/103678

DR FILING DATE: 1998-10-08

DR FILING DATE: 1998-10-08

DR APPLICATION NUMBER: 60/103711

DR APPLICATION NUMBER: 60/103711

DR APPLICATION NUMBER: 60/103711

DR APPLICATION NUMBER: 60/105000

DR FILING DATE: 1998-10-20 APPLICATION NUMBER: 60/090246 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090444 PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090688
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25 FILING DATE: 1998-06-26
APPLICATION UNBER: 60/091628
FILING DATE: 1998-07-05
APPLICATION NUMBER: 60/096012 PRIOR APPLICATION NUMBER: 60/101475
PRIOR FILING DATE: 1998-09-23
PRIOR PLILING DATE: 1998-09-24
PRIOR PLILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101743
PRIOR PILING DATE: 1998-09-24 FILING DATE: 1998-08-10 APPLICATION NUMBER: 60/096757 FILING DATE: 1998-08-17 APPLICATION NUMBER: 60/096949 APPLICATION NUMBER: 60/097979 FILING DATE: 1998-08-26 APPLICATION NUMBER: 60/098749 FILING DATE: 1998-09-01 APPLICATION NUMBER: 60/100662 FILING DATE: 1998-09-16 APPLICATION NUMBER: 60/100683 APPLICATION NUMBER: 60/090862 APPLICATION NUMBER: 60/100930 FILING DATE: 1998-09-17 PRIOR APPLICATION NUMBER: 60/101916 PRIOR FILING DATE: 1998-09-24 PRIOR APPLICATION NUMBER: 60/102570 PRIOR FILING DATE: 1998-09-30 APPLICATION NUMBER: 60/099741 FILING DATE: 1998-09-17 APPLICATION NUMBER: 60/100684 FILING DATE: 1998-09-17 APPLICATION NUMBER: 60/101279 FILING DATE: 1998-09-22 APPLICATION NUMBER: 60/103449 FILING DATE: 1998-10-06 APPLICATION NUMBER: 60/105002 FILING DATE: 1998-10-20 FILING DATE: 1998-06-19 FILING DATE: 1998-08-26 FILING DATE: 1998-09-24 PRIOR PRIOR PRIOR PRIOR

R FILING DATE: 1998-10-27

R APPLICATION NUMBER: 60/106030

R FILING DATE: 1998-10-28

R APPLICATION NUMBER: 60/106464

R APPLICATION NUMBER: 60/106856

R APPLICATION NUMBER: 60/106856 PRIOR FILING DATE: 1998-12-16
PRIOR APPLICATION NUMBER: 60/112854
PRIOR FILING DATE: 1998-12-16
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113408
PRIOR APPLICATION NUMBER: 60/113408
PRIOR FILING DATE: 1998-12-22 FILING DATE: 1998-11-17 APPLICATION NUMBER: 60/112419 FILING DATE: 1998-12-15 APPLICATION NUMBER: 60/112422 FILING DATE: 1998-12-22 APPLICATION NUMBER: 60/113430 FILING DATE: 1998-12-23 APPLICATION NUMBER: 60/116843 FILING DATE: 1999-01-22 APPLICATION NUMBER: 60/119285 APPLICATION NUMBER: 60/119525 FILING DATE: 1999-02-10 APPLICATION NUMBER: 60/119549 FILING DATE: 1998-11-03
APPLICATION NUMBER: 60/108807 APPLICATION NUMBER: 60/112853 PRIOR APPLICATION NUMBER: 60/113011 APPLICATION NUMBER: 60/113621 APPLICATION NUMBER: 60/114223 FILING DATE: 1998-12-30 APPLICATION NUMBER: 60/115614 FILING DATE: 1999-01-12 APPLICATION NUMBER: 60/116527 FILING DATE: 1999-02-09
APPLICATION NUMBER: 60/119287 FILING DATE: 1999-02-11 APPLICATION NUMBER: 60/129122 FILING DATE: 1999-04-13 APPLICATION NUMBER: 60/129674 APPLICATION NUMBER: 60/131291 FILING DATE: 1999-04-27 APPLICATION NUMBER: 60/138387 APPLICATION NUMBER: 09/380138 FILING DATE: 1999-08-25 APPLICATION NUMBER: 09/380142 60/120014 FILING DATE: 1999-06-09 APPLICATION NUMBER: 60/144791 APPLICATION NUMBER: 60/169495 APPLICATION NUMBER: 60/191007 FILING DATE: 2000-03-21 FILING DATE: 1999-12-07 APPLICATION NUMBER: 60/175481 APPLICATION NUMBER: 60/199397 APPLICATION NUMBER: 09/380139 APPLICATION NUMBER: 09/311832 APPLICATION NUMBER: 09/380137 FILING DATE: 1998-12-15 FILING DATE: 1998-12-23 FILING DATE: 1999-01-20 FILING DATE: 1999-02-09 1999-02-10 FILING DATE: 1999-04-16 FILING DATE: 1999-07-20 2000-04-25 FILING DATE: 1999-05-14 PRIOR FILING DATE: 2000-01-11 FILING DATE: 1998-08-25 1998-12-1 1999-08-2 FILING DATE: 1999-0. APPLICATION NUMBER: FILING DATE: DATE: FILING PRIOR PRIOR

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P$430RLI
CURRENT APPLICATION NUMBER: U$/10/052,586
CURRENT APPLICATION NUMBER: U$/00/59263
PRIOR APPLICATION NUMBER: 60/059266
PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-00-18
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-24
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PRIOR PILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-29
PRIOR PILING DATE: 1997-10-31
PRIOR PILING DATE: 1997-10-31
                                                                                                        74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
                                                                                                                                                                                                                                                                                                                                                   128 PYLEELHLDDNSVSAVSIEEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRI 187
                                                                                                                                                                                                                                                                                                                                                                                                                        253 STVELEDFKRYKELQRLGLGNNKITDIENGS--LANIPRVREIHLENNKLKKIPSGLPEL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGM 193
                                                                                                                                                                                                                                              194 NALHVLEMSANPLDNNGIEPGAFEGVTVFHIR-IAEAKLTSVPKGLPPTLLELHLDYNKI 252
16.6%; Score 331.5; DB 12; Length 649; 33.0%; Pred. No. 4.1e-20; Live 37; Mismatches 111; Indels 27;
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31 CPSVCRCDAGFIYCNDRFLTSIPTGIPEDATTLYLQNNQI----
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Watanabe, Colin K.
Wood, William I.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                     Best Local Similarity 33.0%
Matches 86; Conservative
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APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
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US-10-052-586-384
     Query Match
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R APPLICATION NUMBER: 60/066120
R FILING DATE: 1997-11-21
R APPLICATION NUMBER: 60/066466
R FILING DATE: 1997-11-24
R FILING DATE: 1997-11-24
R FILING DATE: 1997-11-24
R APPLICATION NUMBER: 60/069335
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R APPLICATION NUMBER: 60/082568
R FILING DATE: 1998-04-21
R FILING DATE: 1998-04-21
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R FILING DATE: 1998-04-22
R FALING DATE: 1998-04-22
R PAPLICATION NUMBER: 60/082704
R FILING DATE: 1998-04-22
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R APPLICATION NUMBER: 60/069870
R FILING DATE: 1997-12-17
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R APPLICATION NUMBER: 60/077450
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APPLICATION UNBABER: 60/081070
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081195
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APPLICATION NUMBER: 60/077632
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APPLICATION NUMBER: 60/077649
FILING DATE: 1998-03-11
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APPLICATION NUMBER: 60/078939
FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/079786
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APPLICATION NUMBER: 60/080194
FILING DATE: 1998-03-31
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APPLICATION NUMBER: 60/080333
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/081049
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APPLICATION NUMBER: 60/081838
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APPLICATION UNMBER: 60/083322
FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/083495
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APPLICATION NUMBER: 60/083496
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APPLICATION NUMBER: 60/083499
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APPLICATION NUMBER: 60/083559
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FILING DATE: 1998-05-05
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APPLICATION NUMBER: 60/084643
                                                                                                                                                                                                                                                         FILING DATE: 1997-12-11
APPLICATION NUMBER: 60/069425
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APPLICATION NUMBER: 60/085573 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085579 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085582 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085700 FILING DATE: 1998-05-22 APPLICATION NUMBER: 60/086486 FILING DATE: 1998-05-22 APPLICATION NUMBER: 60/087098 FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088033
APPLICATION NUMBER: 60/088167
APPLICATION NUMBER: 60/088167 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088326 APPLICATION NUMBER: 60/088655 FILING DATE: 1998-06-09 APPLICATION NUMBER: 60/088722 APPLICATION NUMBER: 60/088740 APPLICATION NUMBER: 60/088876 ICATION NUMBER: 60/089105 APPLICATION NUMBER: 60/086392 APPLICATION NUMBER: 60/088861 FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/C FILING DATE: 1998-06-02 FILING DATE: 1998-05-07 FILING DATE: 1998-05-15 FILING DATE: 1998-05-15 FILING DATE: 1998-05-28 1998-06-05 FILING DATE: 1998-06-04 FILING DATE: 1998-06-10 FILING DATE: 1998-06-12 FILING DATE: 1998-06-1 FILING DATE: 1998-06-1 FILING DATE: PRIOR PRIOR

5 253 STVELEDFKRYKELQRLGLGNNKITDIENGS--LANIPRVREIHLENNKLKKIPSGLPEL 310 74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133 128 PYLEELHLDDNSVSAVSIEEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRI 187 134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGM 193 194 NALHVLEMSANPLDNNGIEPGAFEGVTVFHIR-IAEAKLTSVPKGLPPTLLELHLDYNKI 27; 16.6%; Score 331.5; DB 12; Length 649; 33.0%; Pred. No. 4.1e-20; 37; Mismatches 111; Indels 31 CPSVCRCDAGFIYCNDRFLTSIPTGIPEDATTLYLQNNQI-----CURRENT APPLICATION NUMBER: US/10/028,072 CURRENT FILING DATE: 2001-12-19 PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089538
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/08953
PRIOR APPLICATION NUMBER: 60/08953
PRIOR APPLICATION NUMBER: 60/089908 Sequence 370, Application US/10028072 Publication Wo. US20030004311A1 GENERAL INPERMATION: APPLICANT: Baker, Kevin P. PRIOR APPLICATION NUMBER: 60/056974 PRIOR FILING DATE: 1997-08-26 PRIOR APPLICATION NUMBER: 60/059113 PRIOR FILING DATE: 1997-09-17 PRIOR APPLICATION NUMBER: 60/059115 PRIOR FILING DATE: 1997-09-17 PRIOR APPLICATION NUMBER: 60/049911 PRIOR FILING DATE: 1997-06-18 PRIOR APPLICATION NUMBER: 60/059117 PRIOR FILING DATE: 1997-09-17 PRIOR APPLICATION NUMBER: 60/059122 PRIOR FILING DATE: 1997-09-17 PRIOR APPLICATION NUMBER: 60/089514 311 KYLQIIFLHSNSIARVGVNDF 331 248 N-LRKLYLQDNHINRVPPNAF 267 Sherwood, Steven Smith, Victoria Stewart, Timothy A. Tumas, Daniel Gerritsen, Mary E. Goddard, Audrey Watanabe, Colin K Beresini, Maureen Godowski, Paul J. Gurney, Austin L. Query Match 16.6% Best Local Similarity 33.0% Matches 86; Conservative Desnoyers, Luc Filvaroff, Ellen DeForge, Laura Gao, Wei-Qiang Wood, William APPLICANT: Zhang TITLE OF INVENTION: RESULT 33 US-10-028-072-370 FILE REFERENCE: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT qq Óλ g Qλ g δλ q q

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R APPLICATION NUMBER: 60/063755
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APPLICATION NUMBER: 60/059588
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APPLICATION NUMBER: 60/059836 APPLICATION NUMBER: 60/063082 FILLING DATE: 1997-10-31 APPLICATION NUMBER: 60/063127 FILING DATE: 1997-10-24 APPLICATION NUMBER: 07/00329 APPLICATION NUMBER: 60/063329 FILING DATE: 1997-10-27 APPLICATION NUMBER: 60/063550 FILING DATE: 1997-10-28 APPLICATION NUMBER: 60/063561 FILING DATE: 1997-10-28 APPLICATION NUMBER: 60/063704 FILING DATE: 1997-10-29 APPLICATION NUMBER: 60/063733 FILING DATE: 1997-10-29 FILING DATE: 1997-11-12 APPLICATION NUMBER: 60/065846 FILING DATE: 1997-11-17 FILING DATE: 1998-01-23
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FILING DATE: 1998-02-04
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APPLICATION NUMBER: 60/062250
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R APPLICATION NUMBER: 60/077791

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R APPLICATION NUMBER: 60/07994

R APPLICATION NUMBER: 60/07963

R APPLICATION NUMBER: 60/079663

R APPLICATION DATE: 1998-03-25

R FILING DATE: 1998-02-27 APPLICALLO.
RAPLICATION UNMER: 60/085339
RAPLICATION UNMER: 60/085339
RFILING DATE: 1998-05-13
RAPLICATION NUMBER: 60/085579
TATAC DAIE: 1998-05-15 R FILING DATE: 19/98-06-11 R APPLICATION NUMBER: 60/089532 R FILING DATE: 1998-06-17 R APPLICATION NUMBER: 60/08959 R FILING DATE: 1998-06-17 R APPLICATION NUMBER: 60/089907 R FILING DATE: 1998-06-18 ARYLLING DATE: 1998-05-U,
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APPLICATION NUMBER: 60/084627 APPLICATION DATE: 1998-06-10
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FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081695 FILING DATE: 1998-04-14 APPLICATION NUMBER: 60/081817 FILING DATE: 1998-04-15 FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/083545 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/084600 FILING DATE: 1998-05-22 APPLICATION NUMBER: 60/086430 FILING DATE: 1998-05-28 APPLICATION NUMBER: 60/088026 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088730 APPLICATION NUMBER: 60/088810 FILING DATE: 1998-06-10 FILING DATE: 1998-02-27 APPLICATION NUMBER: 60/079728 APPLICATION NUMBER: 60/081818 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/082999 FILING DATE: 1998-04-24 APPLICATION NUMBER: 60/083322 APPLICATION NUMBER: 60/084637 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/085149 FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/085338 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085697 APPLICATION NUMBER: 60/085704 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/087106 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088741 APPLICATION NUMBER: 60/086414 1998-05-15 1998-06-10 1998-05-22 1998-05-12 FILING DATE: 1998-05 APPLICATION NUMBER: FILING DATE: FILING DATE: FILING DATE: PRIOR
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Genentech, Inc
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Tumas, Daniel
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APPLICANT: Genentec
  LOCATION: (13)
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US-09-905-291A-28
                                                                                   Query Match
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 EDNSLFPTREPRSHFFPFDLFP-----MCPFGCQCYSR-VVHCSDLGLTSVPTNIPFDTR 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                         ch 16.5%; Score 329; DB 9; Length 642; I Similarity 29.1%; Pred. No. 6.6e-20; 98; Conservative 55; Mismatches 146; Indels
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/USO0/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
               PRIOR FILING DATE: 1998-06-19
PRIOR PLILING DATE: 1998-06-19
PRIOR PELLING DATE: 1998-06-23
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PRIOR FILING DATE: 1998-07-01
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Patent No. US20020052308A1
                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/089947
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NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1192
LENGTH: 415
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Matches 98
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids 0S-09-925-301-1192
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                                                                                                                                                                                                                                 76 TYYDPYDPYPTFTYEPYPYGVDEGPAYTYGSPSPPDPRDCPQECDCPPNFPTAMYCDNRN 135
                                                                                                                                                                                                                                                                                                                                                                                              150 KLRRLYLSHNQLSEIPLNLPKSLAEIRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNN 209
                                                                                                                                                                                                                                                                                                                                                                                                                              G---SSMRGLRSLILLDLSYNHLRKVPDGLPSALEQLYMEHNNVYTVPDSYFRGAPKLLY 311
                                                                                                                                                                                                                                                                                                92 LTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKLT--KIHPKAFLTTK 149
                                                                                                                                                                                                                                                                                                                             GIEPGAFEGV-TVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQR 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGLGNNKITDIENGSLA----NIPRVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIA 324
                                                                                                                                                                                               ---CPFGCQC---YSRVVHCSDLG 91
                                                                                                                                             48;
                                                                                         16.2%; Score 323; DB 10; Length 415; 26.4%; Pred. No. 1.2e-19; Live 64; Mismatches 131; Indels 46
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CURRENT APPLICATION NUMBER: US/09/905,291A
CURRENT FILING DATE: 2001-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   366 EFSISSFCTVVDVVNFSKLQVLRLDGNEIK 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325 RVGVNDFCPTVPKMKKSLYSAISLFNNPVK 354
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PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
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Hillan, Kenneth, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Williams, P. Mickey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Paoni, Nicholas F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roy, Margaret Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ferrara, Napoleor
Filvaroff, Ellen
Fong, Sherman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ashkenazi, Avi
Botstein, David
                                                                                                                   Best Local Similarity 26.4 Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wood, William,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gao, Wei-Qiang
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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PRIOR FILING DATE: 2001-11-15
PRIOR PELING DATE: 2001-11-15
PRIOR PELING DATE: 1997-08-26
PRIOR PLILING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR PELING DATE: 1997-09-18
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R APPLICATION NUMBER: 60/066840

R APPLICATION NUMBER: 60/06994

R FILING DATE: 1997-12-16

R APPLICATION NUMBER: 60/074086

R FILING DATE: 1998-02-09

R FILING DATE: 1998-02-09
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APPLICATION NUMBER: 60/063082
FILING DATE: 1997-10-31
APPLICATION NUMBER: 60/063329
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FILING DATE: 1998-08-18
APPLICATION NUMBER: 60/099601
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APPLICATION NUMBER: 60/062285
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APPLICATION NUMBER: 60/062816
FILING DATE: 1997-10-24
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APPLICATION NUMBER: 60/066364
FILING DATE: 1997-11-21
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APPLICATION NUMBER: 60/099803
APPLICATION DATE: 1998-09-10
APPLICATION NUMBER: 60/099811
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APPLICATION UNMBER: 60/100858
FILING DATE: 1998-09-17
APPLICATION NUMBER: 60/101922
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APPLICATION NUMBER: 60/063733
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APPLICATION NUMBER: 60/081049
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APPLICATION NUMBER: 60/095998
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APPLICATION NUMBER: 60/079294
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Timothy A. Stewart
Daniel Tumas
                                                                                                                                                                                                                                                Paul J. Godowski
Austin L. Gurney
Ivar J. Kljavin
Jennie P. Mather
Mary A. Napier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Colin K. Watanabe
P.Mickey Williams
William I. Wood
                                                                                                                                                 Mary E. Gerritsen
Audrey Goddard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nicholas F. Paoni
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                                            Wei-Qiang Gao
Hanspeter Gerber
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APPLICANT:
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Best Local Similarity 27.7%; Pred. No. 1.4e-18;
Matches 79; Conservative 62; Mismatches 109; Indels 35
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PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-09
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR PILING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-20
PRIOR PELING DATE: 1999-11-20
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-07
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Fatent No. US/20020177165A1
GENERAL INFORMATION:
APPLICANT: Avi J. Ashkenazi
APPLICANT: Kevin P. Baker
APPLICANT: David A. Botstein
APPLICANT: Luc Desnoyers
APPLICANT: Dan L. Eaton
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Sherman Fong
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SEQ ID NO 28 LENGTH: 660

TYPE: PRT

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APPLICANT:
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74 CPFGCQCYSRVVHCSDLGLISVPTNIPFDTRMLDLQNNKIKEIKENDFKGLISLYGLILN 133 252 ISTVELEDFKRYKELQRLGLGNNKITD--IENGSLANIPRVREIHLENNKLKKIPSGLPE 309 192 IAVISDMAFONLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPDLPG 251 134 NNKLTKI-HPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKG 192 36 CPSVCRCDRNFVYCNERSLISVPLGIP-------EGVTVLY---LH 71 193 MNALHVLEMSANPLDNNGIEPGAF-EGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNK 35; Length 660; Indels 310 LKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVK 354 ; Pred. No. 1.4e-18; 62; Mismatches 109; DB 9; 15.7%; Score 313.5; 27.7%; Pred. No. 1.4 PRIOR PILLING DATE: 2001-06-01
PRIOR PILLING DATE: 2001-06-01
PRIOR FILLING DATE: 2001-06-19
PRIOR PLICATION NUMBER: PCT/US98/14552
PRIOR FILLING DATE: 1998-07-14
PRIOR PLICATION NUMBER: PCT/US98/18824 PRIOR APPLICATION NUMBER: PCT/US98/25108 PRIOR FILING DATE: 1998-12-01 PRIOR APPLICATION NUMBER: PCT/US98/25190 PRIOR FILING DATE: 1998-11-25 PRIOR APPLICATION NUMBER: PCT/US99/05028 PRIOR FILING DATE: 1999-03-08 PRIOR APPLICATION NUMBER: PCT/US99/21090 PRIOR FILING DATE: 1999-09-15 FILING DATE: 1998-09-10 APPLICATION NUMBER: PCT/US98/19093 FILING DATE: 1998-09-14 PCT/US98/19330 APPLICATION NUMBER: PCT/US98/19437 PRIOR APPLICATION NUMBER: PCT/US99/12252 LICATION NUMBER: PCT/US99/20111 PRIOR APPLICATION NUMBER: PCT/US99/20594 PRIOR APPLICATION NUMBER: PCT/US99/21547 PCT/US98/24855 PRIOR FILING DATE: 2001-01-22 PRIOR APPLICATION NUMBER: 90/802706 PRIOR FILING DATE: 2001-03-09 PRIOR APPLICATION NUMBER: 09/806689 PRIOR FILING DATE: 2001-03-14 PRIOR PILING DATE: 2001-05-25 RESULT 37 US-09-902-853-28 ; Sequence 28, Application US/09902853 APPLICATION NUMBER: 09/709238 FILING DATE: 2000-11-08 APPLICATION NUMBER: 09/872035 FILING DATE: 2001-06-01 APPLICATION NUMBER: 09/767609 PRIOR APPLICATION NUMBER: 09/870574 PRIOR FILING DATE: 2001-05-30 APPLICATION NUMBER: PCT, FILING DATE: 1998-11-20 1998-09-16 1999-09-08 FILING DATE: 1999-09-01 1999-06-02 1998-09-17 Best Local Similarity 27.7 Matches 79; Conservative APPLICATION NUMBER: FILING DATE: 1998-09 FILING DATE: PRIOR FILING DATE: PRIOR APPL PRIOR FILI PRIOR PRIOR A PRIOR g q g ò QQ ò ò 9

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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: 105/09/902,853
CURRENT FILING DATE: 2001-07-10
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PRIOR APPLICATION NUMBER: US/09/065,350
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 1990-07-07
PRIOR FILING DATE: 1990-07-07
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR PELING DATE: 1990-07-07
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PELING DATE: 1990-07-28
PRIOR PELING DATE: 1990-09-08
PRIOR PELING DATE: 1990-09-08
PRIOR PELING DATE: 1999-09-18
PRIOR PELING DATE: 1999-09-18
PRIOR PELING DATE: 1990-09-18
PRIOR PELING DATE: 1990-09-15
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PELING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-03
PRIOR PELING DATE: 1999-12-03
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PRIOR PELING DATE: 1999-12-03
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Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Pan, James
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Stewart, Timothy A.
Publication No. US20020192659A1
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Goddard, A.
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                                                 APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botsteln, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
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US-09-902-853-28
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LENGTH: 660
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134 NNKLTKI-HPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKG 192
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                                                                                                           Gaps
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        15.7%; Score 313.5; DB 9; Length 660; 27.7%; Pred. No. 1.4e-18; Live 62; Mismatches 109; Indels 35
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CURRENT APPLICATION NUMBER: US/09/907,824
CURRENT FILING DATE: 2001-07-17
RIOR PELICATION NUMBER: US/09/907,824
CURRENT FILING DATE: 2000-09-18
PRIOR PELICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: DS 00/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Pan, James
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Wood, William, I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ferrara, Napoleone
Filvaroff, Ellen
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Gerber, Hanspeter
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Query Match
Best Local Similarity 27.7%;
Matches 79; Conservative
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APPLICANT: Ashkenzi, Avi
APPLICANT: Botstein, David
APPLICANT: Beton, Luc
APPLICANT: Eaton, Dan L.
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APPLICANT:
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Grimaldi, Christopher J.
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                                                                                               Kljavin, Ivar J.
Mather, Jennie P.
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Best Local Similarity 27.7%;
Matches 79; Conservative
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Best Local Similarity 27.7%; Pred. No. 1.4e-18;
Matches 79; Conservative 62; Mismatches 109; Indels 35
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                                                   PRIOR FILING DATE: 1999-0915
PRIOR FILING DATE: 1999-0915
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-16
PRIOR PLICATION NUMBER: PCT/US99/23089
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
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PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-07
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FILLING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E.
Goddard, A.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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US-09-907-824-28
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US-09-907-841-28
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PRIOR PLILING DATE: 2000-02-22
PRIOR PLILING DATE: 2000-02-22
PRIOR PLILING DATE: 1999-07-07
PRIOR PLILING DATE: 1999-07-07
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PRIOR FILING DATE: 1999-09-09
PRIOR PLILOR DATE: 1999-09-09
PRIOR PLILING DATE: 1999-09-09
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PRIOR PLILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PLILING DATE: 1999-09-15
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CURRENT APPLICATION NUMBER: US/09/907,841
                                                                                                                          Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
Gurney, Austin L.
Hillan, Kenneth, J.
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                                                                                                                                                                                                                                                         Godowski, Paul J.
Grimaldi, Christopher J.
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Williams, P. Mickey
Wood, William, I.
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Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
                                                           Ferrara, Napoleone
Filvaroff, Ellen
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Paoni, Nicholas F.
No. US20030003530A1
                                                                            Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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                                                                                                                                       Gurney, Austin L.
                        Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
                 APPLICANT: Genentech, Inc.
                                                   Eaton, Dan L.
                                                                                                             Goddard, A.
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ORGANISM: Homo Sapien
       GENERAL INFORMATION:
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                                                                                                                                                                                                              193 MNALHVLEMSANPLDNNGIEPGAF-EGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNK 251
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                                                                                                                                                                                                                                                                                                                                                                                                              192 IAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPDLPG 251
                                                                                                                           35;
  Length 660;
                                                 Indels
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15.7%; Score 313.5; DB 9; 27.7%; Pred. No. 1.4e-18; Live 62; Mismatches 109;
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PRIOR APPLICATION NUMBER: 60/059113
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059122
PRIOR PILING DATE: 1997-09-17
PRIOR PAPLICATION NUMBER: 60/059122
PRIOR PELING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PAPLICATION NUMBER: 60/059263
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APPLICATION NUMBER: 60/059352
FILING DATE: 1997-09-19
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Stewart, Timothy A.
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Filvaroff, Ellen
Gao, Wel-Qiang
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Gurney, Austin L.
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                                                 Conservative
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                       Best Local Similarity
Matches 79; Conserv
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    Query Match
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APPLICANT:
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APPLICANT:
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R APPLICATION NUMBER: 60/063755
R FILING DATE: 1997-10-17
R PRILIGATION NUMBER: 60/064248
R FILING DATE: 1997-11-03
R APPLICATION NUMBER: 60/064809
R FILING DATE: 1997-11-17 FILING DATE: 1997-11-21
APPLICATION NUMBER: 60/066453
FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/066511
FILING DATE: 1997-11-24 FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/069212
FILING DATE: 1997-12-11
APPLICATION NUMBER: 60/069278 ICATION NUMBER: 60/078910 FILING DATE: 1997-10-24 APPLICATION NUMBER: 60/062816 FILING DATE: 1997-10-27 APPLICATION NUMBER: 60/063329 FILING DATE: 1997-10-27 APPLICATION NUMBER: 60/063550 FILING DATE: 1997-10-29 APPLICATION NUMBER: 60/063733 FILING DATE: 1997-10-29 APPLICATION NUMBER: 60/063735 FILING DATE: 1997-10-29 APPLICATION NUMBER: 60/063738 FILING DATE: 1997-10-29 APPLICATION NUMBER: 60/066770 FILING DATE: 1997-12-11 APPLICATION NUMBER: 60/069694 FILING DATE: 1997-12-16 APPLICATION NUMBER: 60/072320 FILING DATE: 1998-01-23 FILING DATE: 1998-01-23 APPLICATION NUMBER: 60/073612 APPLICATION NUMBER: 60/074086 FILING DATE: 1998-02-09
APPLICATION NUMBER: 60/074092 FILING DATE: 1998-02-09 APPLICATION NUMBER: 60/07791 FILING DATE: 1997-10-17 APPLICATION NUMBER: 60/062814 APPLICATION NUMBER: 60/063045 FILING DATE: 1997-10-31 APPLICATION NUMBER: 60/063127 FILING DATE: 1997-10-24 APPLICATION NUMBER: 60/063327 APPLICATION NUMBER: 60/063561 FILING DATE: 1997-12-11 APPLICATION NUMBER: 60/069334 APPLICATION NUMBER: 60/059836 APPLICATION NUMBER: 60/062285 FILING DATE: 1997-10-17 APPLICATION NUMBER: 60/062287 APPLICATION NUMBER: 60/063082 FILING DATE: 1997-10-28 APPLICATION NUMBER: 60/063704 APPLICATION NUMBER: 60/079294 1998-02-04 998-03-12 1998-03-20 1997-10-24 1997-10-24 FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: PRIOR PRIOR

PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 19/88-66-11
PRIOR FILING DATE: 19/88-66-17
PRIOR FILING DATE: 1998-66-17
PRIOR APPLICATION NUMBER: 60/08959
PRIOR APPLICATION NUMBER: 60/089997
PRIOR PILING DATE: 1988-66-18
PRIOR APPLICATION NUMBER: 60/08997
PRIOR APPLICATION NUMBER: 60/08997
PRIOR APPLICATION NUMBER: 60/08997
PRIOR APPLICATION NUMBER: 60/08987 APPLICATION NUMBER: 60/079663 FILING DATE: 1998-02-27 APPLICATION NUMBER: 60/079728 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/080165 FILING DATE: 1998-03-31 APPLICATION NUMBER: 60/081203 FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/083322 FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/083545 FILING DATE: 1998-04-14 APPLICATION NUMBER: 60/081817 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081818 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/084600 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/085149 FILING DATE: 1998-05-12 APPLICATION NUMBER: 60/085338 FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/085339 FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/085579 APPLICATION NUMBER: 60/086430 FILING DATE: 1998-05-22 APPLICATION NUMBER: 60/087106 FILING DATE: 1998-05-28 APPLICATION NUMBER: 60/088026 PRIOR APPLICATION NUMBER: 60/090349 PRIOR FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090445 FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/081229 FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/081695 APPLICATION NUMBER: 60/082999 APPLICATION NUMBER: 60/084627 APPLICATION NUMBER: 60/084637 APPLICATION NUMBER: 60/085323 APPLICATION NUMBER: 60/085697 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085704 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/086414 APPLICATION NUMBER: 60/088730 APPLICATION NUMBER: 60/088741 FILING DATE: 1998-06-10 60/088810 1998-06-10 APPLICATION NUMBER: 60/C FILING DATE: 1998-06-24 PRIOR FILING DATE: 1998-06-24 FILING DATE: 1998-06-04 FILING DATE: 1998-06-10 FILING DATE: 1998-03-25 FILING DATE: 1998-04-29 FILING DATE: 1998-05-07 1998-05-07 FILING DATE: 1998-04-2 1998-05-2 1998-05-1 1998-05-APPLICATION NUMBER: FILING DATE: 1998-06 FILING DATE: FILING DATE: FILING DATE: FILING DATE: PRIOR PRIOR

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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.7%; Score 313.5; DB 9; Length 660; 27.7%; Pred. No. 1.4e-18; tive 62; Mismatches 109; Indels 35;
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                                                                                                                                                                                                                                                                                           FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,320
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
                                                                                   PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
               FILING DATE: 1998-06-24
APPLICATION UNMBER: 60/090863
FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/091360
APPLICATION NUMBER: 60/090538
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Paoni, Nicholas F.
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Goddard, A.
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                                                                                                                                                                                   Best Local Similarity 27.79
Matches 79; Conservative
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Gao, Wei-Qiang
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                                                                                                                                                                                                Query Match
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134 NNKLTKI-HPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKG 192
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            PRIOR PELING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PELING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/2814
PRIOR PELING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PELING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR PILING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-03
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PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
APPLICATION NUMBER: US 60/143,048
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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US-09-909-320-28
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LENGTH: 660
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us-09-944-457-2.rapb

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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PRIOR APPLICATION NUMBER: PCI/US99/30095
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PRIOR APPLICATION NUMBER: PCT/US99/30911
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PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
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PRIOR FILING DATE: 2000-01-05
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
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Roy, Margaret Ann
                                                                                                                                                                                                                               Gerritsen, Mary E.
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                                                                                                                                                                                       Gerber, Hanspeter
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Best Local Similarity 27.7%
Matches 79; Conservative
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                                                                                                                                                        Gao, Wei-Qiang
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                                                                                                                                                                                                                                                          Goddard, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pan, James
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APPLICANT: Rajput, Bhanu
TITLE OF INVENTION: Human Slit Polypeptide and Polynucleotides Encoding
TITLE OF INVENTION: Same
                                                                                                                                                                                                                                                                  73 CPRVCSCTGLNVDCSHRGLTSVPRKISADVERLELQGNNLTVIYETDFQRLTKLRMLQLT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 NNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLP 169
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                                                                                                                                                                252 ISTVELEDFKRYKELQRIGLGNNKITD--IENGSLANIPRVREIHLENNKLKKIPSGLPE 309
                                                                                                                                        193 MNALHVLEMSANPLDNNGIEPGAF-EGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNK 251
                                              134 NNKLTKI-HPKAFLTTKKLRRLYLSHNQLSEIPLNLPRSLAELRIHENKVKKIQKDTFKG 192
                                                                                          72 NNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTISRAALAQ 131
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---EGVTVLY---LH 71
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CURRENT APPLICATION NUMBER: US/10/011,064
CURRENT FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 60/063,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/096,420
PRIOR FILING DATE: 1998-08-13
36 CPSVCRCDRNFVYCNERSLTSVPLGIP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/10011064
Patent No. US20020123104A1
GENERAL INFORMATION
APPLICANT: Connolly, Timothy
APPLICANT: Rajput, Bhanu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Drosophila melanogaster US-10-011-064-5
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62; Mismatches 109; Indels

74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133

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Godowski, Paul J. Gurney, Austin L.

Goddard, Audrey

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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430RL642
CURRENT APPLICATION NUMBER: US/10/174,590
CURRENT APPLICATION NUMBER: US/10/174,590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 NNKLIKIHPKAFLITKKLRRLYLSHNQLSEIPLNLPKS---LAELRIHENKVKKIQKDTF 190
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209 TLRLHSNHLYCDCHLAWLSDWLRQRRTVGQFTLCMAPVHLRGFNVADVQKKEYVCPAPHS 268
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421 SLLSLYDNNIQ--SLANGTFDAMKSMKTVHL 449
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GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
                                                                               ; Sequence 290, Application US/10174590; Publication No. US20030008352A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                             Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
                                                                                                                                                                          Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                       APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
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Best Local Similarity
                                                  RESULT 45
US-10-174-590-290
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APPLICANT: Watanabe, COLLU N.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACLDS ENCOING THE SAME
FILE REFERENCE: P430R1C1104
CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT PILLING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 290
LENGTH: 1523
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.5%; Score 309; DB 9; Length 1523;
24.9%; Pred. No. 9.6e-18;
Live 58; Mismatches 114; Indels 124; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 CPTKCTCSAASVDCHGLGLRAVPRGIPRNAERLDLDRNNITRITKMDFAGLKNLRVLHLE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209 TLRLHSNHLYCDCHLAWLSDWLRQRRTVGQFTLCMAPVHLRGFNVADVQKKEYVCPAPHS
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Publication No. US20030013153A1
GENERAL INFORMATION:
Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
Zhang, Zemin
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Watanabe, Colin K.
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 24.9%
Matches 98; Conservative
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Godowski, Paul J.
Gurney, Austin L.
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Desnoyers, Luc
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                        154 RGITDVKNLQ-----LDNNHISCIEDGAFRALRDLEILTLNNNNISRILVTSFNHMPKIR 208
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      34 CPTKCTCSAASVDCHGLGLRAVPRGIPRNAERLDLDRNNITRITKMDFAGLKNLRVLHLE 93
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PRIOR FILING DATE: 1977-09-18
PRIOR PELING DATE: 1977-09-18
PRIOR PELING DATE: 1977-09-18
PRIOR PELING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR APPLICATION NUMBER: 60/063486
PRIOR APPLICATION NUMBER: 60/063540
PRIOR PELING DATE: 1997-10-28
PRIOR PELING DATE: 1997-10-28
PRIOR PAPLICATION NUMBER: 60/063541
PRIOR PLING DATE: 1997-10-28
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PRIOR APPLICATION NUMBER: 60/C
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PRIOR APPLICATION NUMBER: 60/C
PRIOR FILING DATE: 1997-10-29
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Wood, William I.
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APPLICANT: Baker, Kevin P.
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24.9%; Pred. No. 9.6e-18;
Live 58; Mismatches 114; Indels 124; Gaps
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CURRENT APPLICATION NUMBER: US/10/175,737
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 290
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Best Local Similarity 24.9%
Matches 98; Conservative
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ORGANISM: Homo sapiens
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; ORGANISM: Homo Sapien
US-10-175-737-290
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US-10-011-064-2
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PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PLILING DATE: 1997-11-13
PRIOR PLILING DATE: 1997-11-21
PRIOR PAPLICATION NUMBER: 60/06947
PRIOR PLILING DATE: 1997-11-21
PRIOR PAPLICATION NUMBER: 60/077450
PRIOR PLILING DATE: 1997-12-17
PRIOR PLILING DATE: 1997-12-17
PRIOR PLILING DATE: 1998-03-11
PRIOR PLILING DATE: 1998-04-09
PRIOR PLILING DATE: 1998-03-11
PRIOR PLILING DATE: 1998-03-12
PRIOR PLILING DATE: 1998-03-13
PRIOR PLILING DATE: 1998-04-09
PRIOR PLILING DATE: 1998-04-15
PRIOR PLILING DATE: 1998-04-29
PRIOR PLILING DATE

R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088655
R APPLICATION NUMBER: 60/088722
R APPLICATION NUMBER: 60/088728
R FILING DATE: 1998-06-10
R FILING DATE: 1998-06-10
R FILING DATE: 1998-06-10
R PILING DATE: 1998-06-10 R APPLICATION NUMBER: 60/084643
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/085573
R FILING DATE: 1998-05-15
R FILING DATE: 1998-05-15
R FILING DATE: 1998-05-18
R FILING DATE: 1998-05-18 APFLICATION DATE: 1998-U3-22
APPLICATION NUMBER: 60/086486
TITMA DATE: 1998-05-22 FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087827
FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088025 FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088167
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088202 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088212 FILING DATE: 1998-06-05 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088811 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088824 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088825 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088826 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/089090 FILING DATE: 1998-06-12 APPLICATION NUMBER: 60/089105 FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085700
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/086023 FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088029
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088033 APPLICATION NUMBER: 60/088217 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088326 FILING DATE: 1998-06-04 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088861 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088863 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088876 FILING DATE: 1998-06-12 APPLICATION NUMBER: 60/089512 APPLICATION NUMBER: 60/086392 FILING DATE: 1998-05-22 FILING DATE: 1998-05-22 APPLICATION NUMBER: 60/087098 FILING DATE: 1998-05-28 APPLICATION NUMBER: 60/087609 FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/087759 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088028 APPLICATION NUMBER: 60/085582 APPLICATION NUMBER: 60/087208 1998-05-18 1998-05-28 1998-06-12 1998-05-15 FILING DATE: FILING DATE: FILING DATE: PRIOR
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Publication No. US20020182638A1

GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff Ellen
APPLICANT: Geritisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimald, Christopher J.
APPLICANT: Watanabe, Colin K.
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                                                                                                                                                                                                                                                                                                                             Query Match 15.5%; Score 309; DB 12; Length 1523; Best Local Similarity 24.9%; Pred. No. 9.6e-18; Matches 98; Conservative 58; Mismatches 114; Indels 124;
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Pred. No. 5.5e-18;
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PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR PRICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR APPLICATION NUMBER: 60/089598
PRIOR PRILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089908
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28.8%;
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US-10-063-547-124
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US-10-063-547-124
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LENGTH: 513
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                                                                                                                                                                                                                                                                                                                     134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGM 193
53; Gaps
                                                  87; Conservative 57; Mismatches 105; Indels
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Job time : 19 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

January 24, 2003, 12:24:51; search time 21 Seconds (without alignments) 1734.997 Million cell updates/sec Run on:

US-09-944-457-2 1992 1 MKEYVLLIFLALCSARPFFS......PATFRCVLSRMSVQLGNFGM 379 Title: Perfect score: Sequence:

283224 seqs, 96134422 residues Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	•	biglycan precursor		biglycan precursor						Ω						7		MEGF5 protein - ra	n	fibromodulin precu		protein 1	cell memb			insulin-like growt	neuronal leucine-r	_	qp150 protein - fr	ple
SUMMAKIES	ID		532/93	S20811	BGHUN	832559	S24317	NBHUC8	S06280	147020	A55454	S29145	A41748	A46743	S52284	139068	805390	S71876	T13953	T42218	S55275	B36665	A36665	A58532	A53860	T42626	JC1282	JC7763	JC6128	T13174	JG0193
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	Score		1040.0	1037.5	1034	1024.5	696	963.5	943	941	907.5	899	399.5	384	378	358.5	342.5	333.5	324	323	318	316	316	296	294	282.5	272	266	265		261.5
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13.1 680 2		12.6 907 2	12.5 322 2							•			11.2 594 2						10.9 1119 2	10.8 1535 2
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## ALIGNMENTS

an precursor - rat  an precursor - rat  trate names: dermatan sulfate proteoglycan I (DS-PGI); proteogles: Rattus norvegicus (Norway rat)  1.02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 20-8  ssion: S32793  ssion: S32793  str K.L.; Asundi, V.; Matzura, D.; Cowan, K.  . Cell Biol. 53, 296-304, 1990  e. Vascular smooth muscle biglycan represents a highly conservance number: S3799; MUID:91184222; PMID:2081845  subsion: S32793; MUID:91184222; PMID:2081845  subsion: S32793; MUID:91184222; PMID:2081845  subsion: S32793  subsion: S32793  subsion: S32793  subsion: S32793  MUID:91184222; PMID:2081845  subsion: S32793  subsion: Sa2793  subsion: Subsion: Sa2793  subsion: Subsion: Sa2793  subsion: Subsion: Sa2793  subsion: Subsio	RESULT S32793	JLT 1 93
C.Species Rattus norvegicus (Norway rat) C.Species Rattus norvegicus (Norway rat) C.Species (2-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 20-Aug-1999 R.Dreber, K.L.; Asundi, 94. Matzura, D.; Cowan, K. Eur. J. Cell Biol. 33, 286-304, 1990 A.Title: Wascular smooth muscle biglycan represents a highly conserved prote A.Refierence number: Sa2793; MUID:9118422; PMID:2081545 A.Accession: Sa2793 A.Molecule type: mRRM A.Molecule type: mRRM A.Residues: 1.56 ADE: A.Cooss-references: GB:017834; NID:9600497; PIDN:AAAS8797.1; PID:9600498 C.Cooss-references: GB:017834; NID:9600497; PIDN:AAAS8797.1; PID:9600498 C.Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; C.Keywords: chondroitin sulfate proteodylycan; dermatan sulfate; extracellulate C.Keywords: chondroitin sulfate proteodylycan; dermatan sulfate; extracellulate F38-82.Domain: proteodylycan #status predicted <810-5 F:116-1397.Domain: perched-fich alpha-2-glycoprotein repeat homology <a <a="" alpha-2-glycoprotein="" domain:leucine-rich="" homology="" href="http://domain.neucine-rich alpha-2-glycoprot&lt;/td&gt;&lt;td&gt;bigl&lt;br&gt;N;Al&lt;/td&gt;&lt;td&gt;lycan precursor - rat&lt;br&gt;Lternate names: dermatan sulfate proteoglycan I (DS-PGI); proteoglycan I core prot&lt;/td&gt;&lt;/tr&gt;&lt;tr&gt;&lt;td&gt;R; Dreher, K.L.; Asundi, V; Matzura, D.; Cowan, K. Eur. J. Cell Biol. 53, 296-304, 1990  A.Title: Vascular smooth muscle biglycan represents a highly conserved prote A; Reference number: 832793; MUID:9118422; PMID:2081545  A; Accession: S32793  A; Status: Preliminary  A; Molecule type: mRNA  A; Residues: 1-369 CNRE  A; Cross-references: 18:017834; NID:9600497; PIDN:AAA58797.1; PID:9600498  C; Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; F C; Rewpords: chondroitin sulfate proteoglycan: dermatan sulfate; extracellula F; 1-16, Domain: propeptide *status predicted &lt;*RRO&gt; F; 17-37, Domain: propeptide *status predicted &lt;*RRO&gt; F; 18-369, Troduct: Diglycan amino-terminal homology &lt; CRRIPS F; 11-16, Domain: proteoglycan amino-terminal homology &lt; CRRIPS F; 11-19, Domain: proteoglycan amino-terminal homology &lt; CRRIPS F; 11-19, Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt; CRRIPS F; 11-19, Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt; CRRIPS F; 11-19, Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt; CRRIPS F; 11-10, Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt; CRRIPS F; 121-234, Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt; CRRIPS F; 121-234, Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt; CRRIPS F; 121-234, Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt; CRRIPS F; 131-334, Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt; CRRIPS F; 131-334, Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt; CRRIPS F; 131-334, Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt; CRRIPS F; 131-334, Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt; CRRIPS F; 131-334, Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt; CRRIPS F; 131-334, Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt; CRRIPS F; 131-334, Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt; CRRIPS F; 131-334, Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt; CRRIPS F; 131-334, Domain: leu&lt;/td&gt;&lt;td&gt;C; SF&lt;br&gt;C; Da&lt;br&gt;C; AC&lt;/td&gt;&lt;td&gt;&lt;/td&gt;&lt;/tr&gt;&lt;tr&gt;&lt;td&gt;A.Title: Vascular smooth muscle biglycan represents a highly conserved prote A.Title: Vascular smooth muscle biglycan represents a highly conserved protection: \$32793.  A.Stecession: \$32793  A.Molecule type: mRNA  A.Restides: 1:366  A.Stecine type: mRNA  A.Restides: 1:366  C.Superfamily: decorin. leucine-rich alpha-2-glycoprotein repeat homology; prof. Sp. 11-165  C.Steverds: Chondroitin Sulfate predicted &lt;SIGS  F.11-370  F.11-370  F.13-1-370  F.13-1-370  F.13-1-370  F.13-1-370  F.13-1-370  F.13-1-370  F.13-1-370  F.13-1-370  F.13-1-370  F.13-1-30  F.13-1&lt;/td&gt;&lt;td&gt;R; Dr&lt;br&gt;Eur.&lt;/td&gt;&lt;td&gt;reher, K.L.; Asundi, V.; Matzura, D.; Cowan, K.&lt;br&gt;. J. Cell Biol. 53, 296-304, 1990&lt;/td&gt;&lt;/tr&gt;&lt;tr&gt;&lt;td&gt;A.Stacussion: S32793 A.Status: preliminary A.Molecule type: mRNA A.Residues: 1-586-CMEN A.Stetus: preliminary A.Molecule type: mRNA A.Stetus: preliminary A.Molecule type: mRNA A.Stetus: 1-586-CMEN C.Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proceedives: chondroitin sulfate status predicted ASIG&gt; C.Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proceedives: chondroit: biglycan *status predicted ASIG&gt; F.13-57/Domain: propeptide *status predicted AND&gt; F.38-359/Product: biglycan *status predicted AND&gt; F.38-359/Product: biglycan *status predicted AND&gt; F.38-36/Domain: proceedy/can amino-terminal homology CARRI&gt; F.38-157/Domain: leucine-rich alpha-2-glycoprotein repeat homology CARRI&gt; F.140-160/Domain: leucine-rich alpha-2-glycoprotein repeat homology CARRI&gt; F.140-160/Domain: leucine-rich alpha-2-glycoprotein repeat homology CARRI&gt; F.140-160/Domain: leucine-rich alpha-2-glycoprotein repeat homology CARRIP F.210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology CARRIP F.231-254/Domain: leucine-rich alpha-2-glycoprotein repeat homology CARRIP F.231-359/Domain: leucine-r&lt;/td&gt;&lt;td&gt;A;Ti&lt;br&gt;A;Re&lt;/td&gt;&lt;td&gt;itle: Vascular smooth muscle biglycan represents a highly conserved proteoglycan w&lt;br&gt;eference number: S32793; MUID:91184222; PMID:2081545&lt;/td&gt;&lt;/tr&gt;&lt;tr&gt;&lt;td&gt;A. Wolceule types mRNA A. Residues: 1-369 cDRE A. Cross-references: GB:017834; NID:9600497; PIDN:AAA58797.1; PID:9600498 C. Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; C. Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; C. Reywords: chondroitin sulfate proteoglycan; dermatan sulfate; extracellula C. Reywords: chondroitin sulfate proteoglycan; dermatan sulfate; extracellula F;11-16/Domain: propeptide status predicted cRND F;38-35/Domain: proteoglycan amino-terminal homology cPAH&gt; F;38-37/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRRD&gt;F;16-139/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRRD&gt;F;16-139/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRRD&gt;F;16-130/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRRD&gt;F;16-130/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRRD&gt;F;20-20/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRD&gt;F;20-20/Domain: leucine-rich alpha-2-glycoprotein repeat homology&lt;/td&gt;&lt;td&gt;A;Ac&lt;br&gt;A;St&lt;/td&gt;&lt;td&gt;ocession: S32793&lt;br&gt;Satus: preliminary&lt;/td&gt;&lt;/tr&gt;&lt;tr&gt;&lt;td&gt;A;Cross-references: GB:U17834; NID:g600497; PIDN:AAA58797.1; PID:g600498 C;Superfamily: decorin; leucine-rich alpha-2-g1ycoprotein repeat homology; C;Superfamily: decorin; leucine-rich alpha-2-g1ycoprotein sulfate; extracellula F;1-16/Domain: signal sequence #status predicted &lt;SIG&gt; F;17-37/Domain: propeptide #status predicted &lt;SIG&gt; F;17-37/Domain: propeptide #status predicted &lt;SIG&gt; F;38-369/Product: biglycan #status predicted &lt;AMT&gt; F;38-369/Product: biglycan #status predicted &lt;AMT&gt; F;38-369/Product: biglycan #status predicted &lt;AMT&gt; F;38-369/Product: biglycan #status predicted CAMT&gt; F;38-369/Product: biglycan #status predicted AMT&gt; F;38-369/Product: leucine-rich alpha-2-glycoprotein repeat homology &lt;LRR3&gt; F;116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt;LRR5&gt; F;210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt;LRR5&gt; F;210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt;LRR9&gt; F;279-301/Domain: leucine-rich alpha-2-glycoprotein repeat homology  //rrs8&gt; F;279-30&lt;/td&gt;&lt;td&gt;A;Mc&lt;br&gt;A;Re&lt;/td&gt;&lt;td&gt;olecule type: mRNA&lt;br&gt;esidues: 1-369 &lt;DRE&gt;&lt;/td&gt;&lt;/tr&gt;&lt;tr&gt;&lt;td&gt;C; Keywords: Chondroitin sulfate proteoglycan; defrmatan sulfate; extracelluid F; 11-16/Domain: signal sequence #status predicted &lt;PIG&gt;F; 17-37/Domain: signal sequence #status predicted &lt;PIG&gt;F; 17-37/Domain: signal sequence #status predicted &lt;PIG&gt;F; 17-37/Domain: signal sequence #status predicted &lt;PIG&gt;F; 18-36/Product: bigiycan #status predicted &lt;PIG&gt;F; 18-36/Product: bigiycan #status predicted &lt;PIG&gt;F; 18-36/Product: bigiycan amino-terminal homology &lt;PIGRS&gt;F; 116-139/Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt;IGRR3&gt;F; 16-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt;IGRR5&gt;F; 16-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt;IGRR5&gt;F; 18-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt;IGRR5&gt;F; 210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt;IGRR5&gt;F; 210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt;IGRR5&gt;F; 210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt;IGRR9&gt;F; 270-301/Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt;IGRR9&gt;F; 271-301/Domain: proteoglycan carboxyl-terminal homology &lt;IGRR9&gt;F; 271&lt;/td&gt;&lt;td&gt;A;Cr&lt;br&gt;C;Su&lt;/td&gt;&lt;td&gt;coss-references: GB:U17834; NID:g600497; PIDN:AAA58797.1; PID:g600498&lt;br&gt;Derfamily: decorin: leucine-rich alpha-2-qlyconrotein remeat homology: proteonlyce&lt;/td&gt;&lt;/tr&gt;&lt;tr&gt;&lt;td&gt;F;17-37/Domain: suguence *Status predicted cPRO&gt; F;18-36/Product: biglycan #status predicted cPRO&gt; F;38-369/Product: biglycan #status predicted cPRO&gt; F;38-369/Product: biglycan #status predicted cAMI&gt; F;38-369/Product: biglycan #status predicted cAMI&gt; F;38-310/Domain: protegolycan amino-terminal homology cPRO&gt; F;38-310/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR3&gt; F;16-139/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR3&gt; F;16-136/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR3&gt; F;16-136/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR5&gt; F;210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR5&gt; F;231-254/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR5&gt; F;231-254/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR5&gt; F;230-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR5&gt; F;230-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR5&gt; F;230-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR5&gt; F;242-48,181,199/Binding site: darboxyl-terminal homology CRCH&gt; F;317-369/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR5&gt; F;242-48,181,199/Binding site: darboxyl-terminal homology CRCH&gt; F;42-48,181,199/Binding site: carboxyl-terminal homology CRCH&gt; F;42-48,181,199/Binding site:&lt;/td&gt;&lt;td&gt;C; Ke&lt;/td&gt;&lt;td&gt;sywords: chondroiting to protectly and dermatan sulfate; extracellular matrix;&lt;/td&gt;&lt;/tr&gt;&lt;tr&gt;&lt;td&gt;F;38-294/Product: Diglycan #Status predicted &lt;a href=" http:="" mailto:="" print"="" repeat="">Mailto: Print alpha-2-glycoprotein repeat homology <a href="Mailto: 134">Mailto: Product: Diglycan amino-terminal homology <a href="Mailto: 134">Mailto: 134</a> F;32-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <a href="Mailto: 134">Mailto: 134</a> F;140-160/Domain: leucine-rich alpha-2-glycoprotein repeat homology <a href="Mailto: 134">Mailto: 134</a> F;160-184/Domain: leucine-rich alpha-2-glycoprotein repeat homology <a href="Mailto: 134">Mailto: 134</a> F;210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology <a href="Mailto: 134">Mailto: 134</a> F;231-254/Domain: leucine-rich alpha-2-glycoprotein repeat homology <a href="Mailto: 134">Mailto: 134</a> F;237-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology <a href="Mailto: 134">Mailto: 134</a> F;237-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology <a href="Mailto: 134">Mailto: 134</a> F;237-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology <a href="Mailto: 134">Mailto: 134</a> F;237-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology <a href="Mailto: 134">Mailto: 134</a> F;237-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology <a href="Mailto: 134">Mailto: 134</a> F;237-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology <a href="Mailto: 134">Mailto: 134</a> F;237-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology <a href="Mailto: 134">Mailto: 134</a> F;237-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology <a href="Mailto: 134">Mailto: 134</a> F;237-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology <a href="Mailto: 134">Mailto: 134</a> F;317-316/Pomain: leucine-rich alpha-2-glycoprotein repeat homology <a href="Mailto: 134">Mailto: 134</a> F;317-316/Pomain: leucine-rich alpha-2-glycoprotein repeat homology <a href="Mailto: 134">Mailto: 134</a> F;317-316/Pomain: leucine-rich alpha-2-glycoprotein repeat homology <a href="Mailto: 134">Mailto: 134</a> F;317-316/Pomai</a></a>	F;17	10/Domain: Signal Sequence *Status predicted <216>
F;92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lrr1> F;18-130/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lrr2> F;140-160/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lrr2> F;140-184/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lrr3> F;161-184/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lrr5> F;210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lrr5> F;210-234/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lrr8> F;231-254/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lrr8> F;270-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lrr8> F;270-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lrr8> F;303-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lrr8> F;303-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lrr8> F;303-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology </lrr8> F;317-369/Domain: leucine-rich alpha-2-glycoprotein repeat homology </lrr8> F;317-312/Momain: leucine-rich alpha-2-glycoprotein repeat homology </lrr8> F;213-11,136/Mainding site: dermatan sulfate (Ser) (covalent) #status predicted  F;211,312/Binding site: dermatan sulfate (Ser) (covalent) #status predicted  Ouery Match  Best Local Similarity 52.6%; Pred. No. 1.2e-63; Matches 19; Conservative 67; Mismatches 93; Indels 19; Gaps Opposite of the sulfate (Ser) (covalent)                                      </lrr8></lrr8></lrr8></lrr5></lrr5></lrr3></lrr2></lrr2></lrr1>	F : 58	3-363/Product: b1g1ycan #status predicted <mat> 3-82/Domain: proteoglycan amino-terminal homology <pah></pah></mat>
F;140-160/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR3-F;140-160/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR3-F;181-184/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR5-F;181-284/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR5-F;210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR5-F;255-278/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR7-F;255-278/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR8-F;279-301/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR8-F;279-301/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR8-F;317-369/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR8-F;317-369/Domain: proteoglycan carboxyl-terminal homology *extatus F;317-369/Domain: proteoglycan carboxyl-terminal homology *extatus F;317-369/Domain: proteoglycan carboxyl-terminal homology *extatus F;327-369/Domain: proteoglycan carboxyl-terminal homology *extatus pred F;271.312/Binding site: carboxyl-terminal homo	F;92	2-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lrri></lrri>
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F;210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR6> F;231-236/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR6> F;235-278/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR7> F;255-278/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR8> F;279-301/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR8> F;279-301/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR8> F;317-369/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR8> F;317-369/Domain: proteoglycan carboxyl-terminal homology *extatus pred F;271,312/Binding site: carbohydrate (Asn) (covalent) *status predicted Query Match  Query Match  52.2%; Score 1040.5; DB 2; Length 369; Best Local Similarity 52.6%; Pred. No. 1.2e-63; Matches 19; Conservative 67; Mismatches 93; Indels 19; Caps  Qy 4 YVLLETALCSARPFFSPSHIALKNWMLKDMEDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD	F;16	11-184/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lrr4></lrr4>
F;231-254/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lrr7> F;255-278/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lrr8> F;279-301/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lrr8> F;279-301/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lrr8> F;317-369/Domain: proteoglycan carboxyl-terminal homology *extatus F;317-369/Domain: proteoglycan carboxyl-terminal homology *extatus F;317-369/Domain: proteoglycan carboxyl-terminal homology *extatus F;271,312/Binding site: carbohydrate (Asn) (covalent) *status pred F;271,312/Binding site: carbohydrate (Asn) (covalent) *status predicted Query Match 52.2%; Score 1040.5; DB 2; Length 369; Best Local Similarity 52.6%; Pred. No. 1.2e-63; Matches 199; Conservative 67; Mismatches 93; Indels 19; Gaps Qy 4 YVLLETALCSARPFFSPSHIALKNWMLKDMEDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD</lrr8></lrr8></lrr8></lrr7>	F; 21	10-230/Domain: leacine-rich alpha-2-glycoprotein repeat homology <pre>cLRR6&gt;</pre>
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0302-316/Domain: leucine-rich alpha-2-jlycoprotein repeat homology 317-369/Domain: proteoglycan carboxyl-terminal homology acPUB-317-369/Domain: proteoglycan carboxyl-terminal homology acPUB-317-312/Binding site: dermatan sulfate (Ser) (covalent) #status predic 271.312/Binding site: carbohydrate (Asn) (covalent) #status predic 271.312/Binding site: carbohydrate (Asn) (covalent) #status predic 20 20 20 20 20 20 20 20 20 20 20 20 20	F; 27	
21.312/Binding site: dermaten sulfate (Ser) (covalent) #status 271.312/Binding site: dermaten sulfate (Ser) (covalent) #status 271.312/Binding site: darbohydrate (Asn) (covalent) #status predicted 271.312/Binding site: carbohydrate (Asn) (covalent) #status 372.2% Score 1040.5; DB 2; Length 369; Best Local Similarity 52.6%; Pred. No. 1.2e-63; Matches 199; Conservative 67; Mismatches 93; Indels 19; Gap 4 YVLLEFLALCSARPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD	F;30	
271,312/Binding site: carbohydrate (Asn) (covalent) *status predicted  Duery Match 52.2%; Score 1040.5; DB 2; Length 369;  Best Local Similarity 52.6%; Pred. No. 1.2e-63;  Matches 199; Conservative 67; Mismatches 93; Indels 19; Gap  4 YVLLEFLALCSARPFFSPSHIALKNMALKDMEDTDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD	F; 42	:/-309/Domain: proceogrycan carboxyl-terminal nomology <pch> /,48,181,199/Binding site: dermatan sulfate (Ser) (covalent) #status predicted</pch>
Duery Match 52.2%; Score 1040.5; DB 2; Length 369; Best Local Similarity 52.6%; Pred. No. 1.2e-63; Matches 199; Conservative 67; Mismatches 93; Indels 19; Ga 4 YULLFLALCSARPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD	F;27	11,312/Binding site: carbohydrate (Asn) (covalent) #status predicted
Matches 199; Conservative 67; Mismatches 93; Indels 19; Ga 4 YULLELALCSARPFFSPSHIALKNAMLKDMEDTDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD	no Be	nery Match 52.2%; Score 1040.5; DB 2; Length 369;
4 YULLELALCSARPFFSPSHIALKNWMLKDMEDTDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD	Ma	
::	Qy	YVLILLFLALCSAKPF FSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDSLFPTR
60 EPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEN [	qq	::
60FSAMCPFGCHCHLRVVQCSDLGLKTVPKEISPDTTLLDLQNNDISELRKD	Qγ	EPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEN
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3;

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A.Molecule type: DNA
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A.Residues: 1-368 <FIS1>
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A.Note: the translated sequence in GenBank entry HUMBGN3, release 113.0, (PIDN:AAA522
A.Note: the translated sequence in GenBank entry HUMBGN3, release 113.0, (PIDN:AAA522
A.Note: the DNA) and 2.6 residues inserted after residue 80 (apparently from a misread s
R.Just, W.; Rau, W.; Muller, R.; Geerkens, C.; Vogel, W.
Hum. Mol. Genet. 3, 2268, 1994
A.Title: Dinucleotide repeat polymorphism at the human biglycan (BGN) locus.
A.Reference number: 138706; MUID:95187185; PMID:7881444
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A; Cross-references: GB:J04599; NID:g184339
A; Cross-references: GB:J04599; NID:g184339
A; Note: parts of this sequence, including the amino end of the mature protein, were d A; Note: the translated sequence in GenBank entry HUMHPG1, release 113.0, (PIDN:AAA360 B; Stoecker, G.; Meyer, H.E.; Wagener, C.; Greiling, H.
Biochem. J. 274, 415-420, 1991
A; Title: Purification and N-terminal amino acid sequence of a chondroitin sulphate/de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        biglycan precursor - human hall the matternate names: cartilage proteoglycan I; dermatan sulfate proteoglycan I (DS-PGI) N;Alternate names: cartilage proteoglycan I; dermatan sulfate proteoglycan I (DS-PGI) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 21-Apr-1992 #sequence_revision 26-May-1995 #text_change 28-Jan-2000 C;Accession: A40757; 138706, A32458; S14349; S05639; A28457 R;Fisher, L.W.; Heegaard, A.M.; Vetter, U.; Vogel, W.; Just, W.; Termine, J.D.; Young J. Blol. Chem. 266, 14371-14377, 1991 A;Tefarence number: A40757; MUID:91317791; PMID:1860845 A;Accession: A40757.
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 361-368 «JUS)
A; Cross-references: EMBL: U11686; NID: g607862; PIDN: AAC50117.1; PID: g619663
A; Cross-references: EMBL: J. D.; Young, M.F.
B; Fisher, L.W.; Termine, J.D.; Young, M.F.
A; Fisher, L.W.; Termine, J.D.; M.F.
A; Fithe: Deduced protein sequence of bone small proteoglycan I (Biglycan) shows homol A; Reference number: A32458; MUID: 89174714; PMID: 2647739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 NKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLP 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 PTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNK 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPRSHEFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEN 119
                                                                                                                                                                                                                                                                                                                                                                                               60 -----FSAMCPFGCHCHLRVVQCSDLGLKTVPKEISPDTTLLDLQUNDISELRKD 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 DFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 LKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQ 359
                                                                                     Gaps
                                                                                                                                                                      4 YVLLIFLALCSAKPF----FSPSHIALKNWMLKDMEDTDDDDDDDDDDDDDDDDDDDFPTR 59
                                                                                                                                                                                                                                                       5 WLLTLLLALSQALPFEQKGFWDFTLDDGLLMMNDEEASGSDTTSGVPDLD----SVTPT- 59
                                                                                     19;
                                                                                     93; Indels
    DB 2;
52.1%; Score 1037.5; DI 52.4%; Pred. No. 2e-63;
                                                                                     68; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATFRCVLSRMSVQLGNF 377
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                                                                                 Matches 198; Conservative
                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A32458
         Query Match
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Cipacession: 320811; As7645; 149534

Cipacession: 320811; As7645; 149534

R.Nation, Y.: Suzuki, S.

Submitted to the EMBL Data Library, July 1990

R.Nation, Y.: Suzuki, S.

Submitted to the EMBL Data Library, July 1990

A.Reference number: S20811

A.Reference number: S20811

A.Reference number: S20811

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A.Re
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homology <LRR8>
homology <LRR8>
homology *Status atypical <LF
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F; 116-139/Domain: leucine-rich alpha-2-glycoprotein repeat homology < CLRR3>
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F; 181-208/Domain: leucine-rich alpha-2-glycoprotein repeat homology < CLRR5>
F; 210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology < CLRR5>
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F; 213-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology < CLRR8>
F; 213-316/Domain: proteoglycan carboxyl-terminal homology </br>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 LKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQ 359
         120 DFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHE 179
                                                                                                                                                                                    180 NKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLP 239
                                                                                                                                                                                                                                                                                                                                                           240 PTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNK 299
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A;Molecule type: mRNA
A;Redidues: 1-67, W',69-369 <RES>
A;Crossreferences: GB:L20276; NID:g348961; PIDN:AAA64360.1; PID:g348962
C;Genetics:
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N;Alternate names: biglycan
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A; Accession: S34229
A; Molecule type: mRNA
A; Residues: 1-250, 'V. 252-369 < MAR>
A; Cross-references: EMBL: L07953
B; Neame, P.J.; Choi, H.U.; Rosenberg, L.C.
J. Biol. Chem. 264, 8653-8661, 1989
A; Title: The primary structure of the core protein of the small, leucine-rich proteog
A; Accession: A33701; MUID: 89255324; PMID: 2656687
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A;Residues: 17-24, F7, 26-30 <MA2>
A;Residues: 17-24, F7, 26-30 <MA2>
A;Residues: 17-24, F7, 26-30 <MA2>
B;Scott, P.G.; Nakano, T.; Dodd, C.M.
Biochim. Biophys. Acta 1244, 121-128, 1995
A;Title: Small proteoglycans from different regions of the fibrocartilaginous temporo A;Reference number: $55673; MUID:95284073; PMID:7766647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 38-41, X', 49-53 <SCO>
C; Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglyc C; Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycor; Residues: cartilage; chondrolitn sulfate proteoglycan; dermatan sulfate; extracellu F:1-16/Domain: signal sequence *status predicted <SIG> *SIG>*SIGNATIONAL Sequence *status predicted <PRO>
F:17-37/Domain: amino-terminal propeptide *status predicted <PRO>
F:18-369/Product: biglycan *status predicted <MAT>
F:58-369/Product: biglycan *status predicted <MAT>
F:59-482/Domain: proteoglycan amino-terminal homology <PAH>
F:52-1157/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:116-1139/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:161-184/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:185-208/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
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A; Residues: 38-187, 'E', 189-367, 'Y' < NEA>
A; Experimental source: cartilage
K; Chol, H.U.; Johnson, T.L.; Pal, S.; Tang, L.H.; Rosenberg, L.; Neame, P.J.
J. Biol. Chem. 264, 2876-2884, 1989
A; Title: Characterization of the dermatan sulfate proteoglycans, DS-PGI and DS-PGII,
A; Reference number: A31430; MUID:89123388; PMID:2914936
A; Recession: A31430
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A; Title: The amino-terminal region of a proteochondroitin core protein, secreted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 38-41, 'X',43-47,'X',49-63 <CHO>
A;Residues: 18-41, 'X',43-47,'X',49-63 <CHO>
A;Note: sequences from skin and cartilage were identical
B;Marcum, J.A.; Thompson, M.A.
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A; Accession: PT0078
                                                                                                                                      351 TFRCVTDRLAIQFGNY 366
                                                          362 TFRCVLSRMSVQLGNF 377
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                                                                                                                                                                                            R;Roùghley, P.J.; White, R.J.
Biochem. J. 262, 823-827, 1989
A;Title: Dermatan sulphate proteoglycans of human articular cartilage. The properties of A;Reference number: S05639; MUID:90073579; PMID:2590169
A;Accession: S05639
                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Molecule type: protein
A; Rsesidues: 38-41, X', 43-46, X', 48-57 <ROU>
A; Residues: 38-41, X', 43-46, X', 48-57 <ROU>
J. Biol. Chem. 262, 9702-9708, 1987
J. Biol. Chem. 262, 9702-9708, 1987
A; Title: Purification and partial characterization of small proteoglycans I and II, bone A; Reference number: A92656; MUID:87250639; PMID:3597437
A; Accession: A28457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Map position: Xq28-Xq28
A; Introns: 80/1; 117/3; 189/1; 226/1; 257/2; 303/3
A; Introns: 80/1; 117/3; 189/1; 226/1; 257/2; 303/3
C; Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan
C; Keywords: chondroitin sulfate proteoglycan; dermatan sulfate; duplication; extracellul
F; 1-16/Domain: signal sequence #status predicted <SIG>
F; 17-37/Domain: propeptide #status predicted <PRO>
F; 38-368/Product: biglycan #status predicted <AMI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 RSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 KGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 VKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLK 301
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A; Reference number: S14349; MUID:91174749; PMID:1848758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Residues: 38 41, 78', 43 - 62, 78', 64 - 66 <FIS3>
A; Experimental source: bone
C; Genetics:
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Matches 200; Conservative
                                                                            A, Molecule type: protein
A, Residues: 38-57 <STO>
A, Experimental source: aorta
                                        A; Accession: S14349
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N;Alternate names: cartilage proteoglycan protein II; DS-PG II; PG40 core protein; pr C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 21-Jan-2000 C;Accession: A45016; A45015; B45015; A26476; S05640 R;Vetter, U; Vogel, W; Just, W; Young, M.F.; Fisher, L.W. Genomics 15, 161-168, 1993
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A. Motes sequence extracted from NCBI backbone (NCBIP:125061)
B. Danielson, K.G.; Fazzio, A.; Cohen, I.; Cannizzaro, L.A.; Eichstetter, I.; Iozzo, R Genomics 15, 146-160, 1993
A. Title: The human decorin gene: intron-exon organization, discovery of two alternating A. Reference number: A45015; MUID:93162642; PMID:8432526
A. Status: not compared with conceptual translation
A. Molecule type: DNA
A. Residues: 28-70 CAD2.
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Proc. Natl. Acad. Scl. U.S.A. 83, 7683-7687, 1986
A;Title: Primary structure of an extracellular matrix proteoglycan core protein deduc
A;Reference number: A26476; MUID:87017013; PMID:3484330
                                                                                               homology #status atypical
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F;268-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR9>
F;291-305/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status
F;306-357/Domain: proteoglycan carboxyl-terminal homology PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 GFG----PVCPPRCQCHLRVVQCSDLGLERVPKDLPPDTTLLDLQNNKITEIREGDFKNL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 ELHLDGNKISKIDAEGLSGLTNLAKLGLSFNSISSVENGSLNNVPHLRELHLNNNELVRV 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 IQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGLPPTLL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATF 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKI 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 FFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 TSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                         5 VLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDFPTREPRSH 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 357;
                                                                                                                                                                                                                                                                                                                                98; Indels
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                                                                                                                                                                                                                                      ); Score 969; DB 2;

); Pred. No. 8.9e-59;

65; Mismatches 98;
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                                                                                                                                                                                                                                                48.6%; Score 969; 50.0%; Pred. No. 8
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.0%
Matches 187; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RCVLSRMSVQLGNF 377
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A;Residues: 296-359 <DAN>
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A; Residues: 1-357 <LIW>A; Molecule type: mRNA
A; Residues: 1-357 <LIW>A; Residues: 1-354.74
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 31-33, /x, /41-48, /x, /50-51 <LIA>
A; Residues: 31-33, /x, /35-39, /x, /41-48, /x, /50-51 <LIA>
A; Residues: 31-33, /x, /35-39, /x, /41-48, /x, /50-51 <LIA>
A; Residues: 31-33, /x, /35-39, /x, /41-48, /x, /50-51 <LIA>
C; Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan
C; Keywords: collagen binding: extracellular matrix; glycoprotein
C; Keywords: collagen binding: extracellular matrix; glycoprotein repeat homology <LRRI>
F; 17-30-103-Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRA>
F; 173-196-Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRS>
F; 173-196-Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRS>
F; 120-243/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRS>
F; 120-245/Domain: 
F;231-254/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;255-278/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;302-310/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;302-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;317-369/Domain: leucine-rich alpha-2-glycoprotein repeat homology «status atypical <LFF) = 242.48/Blainding site: dermatan sulfate (Ser) (covalent) #status experimental F;211,312/Binding site: dermatan sulfate (Ser) (covalent) #status predicted F;271,312/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 LLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 KIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 RSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 ----LPPTYSAMCPFGCHCHLRVVQCSDLGLKAVPKEISPDTTLLDLQNNDISELRKDDF 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 KGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 LLLFLALCSAKPFFSPSHIALKNWMLKDMEDTDDDDD-----DDDDDDDDDDDDDDSLFPTREP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                              51.4%; Score 1024.5; DB 2; Length 369; 52.1%; Pred. No. 1.5e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65; Mismatches
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Fri Jan 24 13:09:55 2003

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decorin precursor - bovine

Nalternate names: dermatan sulfate proteoglycan II; proteoglycan core protein II

C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Aug-1999
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Aug-1999
C;Accession: S06280; B31430; A26545; A20935
R;Day, A.A.; McQuillan, C.I.; Termine, J.D.; Young, M.R.
Biochem, J. 248, 801-805, 1987
A;Title: Molecular cloning and sequence analysis of the cDNA for small proteoglycan I
A;Reference number: S06280; MUID:88133946; PMID:3435485
A;Mocession: S06280
A;Mocession: S06280
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A; Residues: 31-33, X', 35-54 <CHO>
A; Residues: 31-33, X', 35-54 <CHO>
A; Residues: 31-33, X', 35-54 <CHO>
A; Coster, L.; Rosenberg, L.C.; van der Rest, M.; Poole, A.R.
J. Biol. Chem. 262, 3809-3812, 1987
A; Title: The dermatan sulfate proteoglycans of bovine sclera and their relationship the A; Reference number: A26545; MUID:87137687; PMID:3818667
A; Accession: A26545
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A; Residues: 31-54 < PEBA>
A; Reperimental source: skin
B; Chopra, R.K.; Pearson, C.H.; Pringle, G.A.; Fackre, D.S.; Scott, P.G.
B; Chopra, R.K.; Pearson, C.H.; Pringle, G.A.; Fackre, D.S.; Scott, P.G.
B; Chopra, R.K.; Pearson, C.H.; Pringle, G.A.; Fackre, D.S.; Scott, P.G.
B; Chopra, R.K.; Pearson, C.H.; Pringle, G.A.; Fackre, D.S.; Scott, P.G.
B; Chopra, R.K.; Pearson, C.H.; Pringle, G.A.; Pearson, G.B.; Pringle, G.G.; Pringle, F.G.; Pringle, G.G.; Pring
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A; Title: Characterization of the dermatan sulfate proteoglycans, DS-PGI and DS-PGII, A; Reference number: A31430; MUID:89123388; PMID:2914936
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A; Residues: 31-50 (-COS>
A; Experimental source: sclera
R; Pearson, C.H.; Winterbottom, N.; Fackre, D.S.; Scott, P.G.; Carpenter, M.R.
J. Balol. Chem. 258, 15101-15104, 1983
A; Reference number: A20935; MUID:84087911; PMID:6654908
A; Accession: A20935
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A;Cross_references: EMBL:Y00712; NID:9618; PIDN:CAA68702.1; PID:9619
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Matches 186; Conserv
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                                                                                                                                                 A,Cross-references: GB:M14219; NID:g181169; PIDN:AAB00774.1; PID:g181170
R;Roughley, P.J.; White, R.J.
Biochem. J. 262, 823-827, 1989
A;Title: Dermatan sulphate proteoglycans of human articular cartilage. The properties of A;Reference number: S05639; MUID:90073579; PMID:2590169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Map position: 12921.3-12933
A:Introns: 71/1; 108/3; 180/1; 218/1; 249/2; 295/3
C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan C:Keywords: chondroitin sulfate proteoglycan; collagen binding; dermatan sulfate; duplic F:1-16/Domain: signal sequence #status predicted <SIG> F:17-30/Domain: propeptide #status predicted <PRO> F:31-359/Product: decorin #status predicted <PRO> F:31-359/Product <PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
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F;34/Binding site: dermatan sulfate (Ser) (covalent) #status experimental
F;189,325/Binding site: dermatan sulfate (Ser) (covalent) #status predicted
F;211,262,303/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F)82-105/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR1>
F)106-129/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR2>
F)130-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR3>
F)151-174/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR4>
F)151-174/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR4>
F)201-221/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR6>
F)22-245/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR6>
F)246-256/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR8
F)293-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR8
F)203-256/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 EPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 DFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 NKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENN 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 KLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEM 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 -----FEPSLGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNNKTTEIKDG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.4%; Score 963.5; DB 1; Length 359; 50.4%; Pred. No. 2.1e-58;
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Best Local Similarity 50.4%; Pred. No. 2.1e-20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;48-72/Domain: proteoglycan amino-terminal homology <PAH>
                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S05640
A; Molecule type: protein
A; Residues: 31-33,'X',35-50 <ROU>
C; Comment: This protein binds type I collagen.
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GDB:119839; OMIM:125255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||:||||| | ::||||:
QPSTFRCVYVRSAIQLGNY 358
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                                                  A; Molecule type: mRNA
A; Residues: 1-359 <KRU>
A; Accession: A26476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: GDB: DCN
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RESULT 7

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A; Cross-references: EMBL.X53929; NID:953668; PIDN:CAA37876.1; PID:953669
C; Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglyc C; Keywords: collagen binding; extracellular matrix; glycoprotein C; Keywords: collagen binding; extracellular matrix; glycoprotein E;1.16/Domain: signal sequence #status predicted <81G>
F;1.16/Domain: propeptide #status predicted <PRO>
F;43.67/Domain: proteoglycan amino-terminal homology <PAH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C,Accession: A55454; S20812
C,Accession: A55454; S20812
R;Scholzen, T.; Solursh, M.; Suzuki, S.; Reiter, R.; Morgan, J.L.; Buchberg, A.M.; Si
J. Biol. Chem. 269, 28270-28281, 1994
A;Title: The murine decorin. Complete cDNA cloning, genomic organization, chromosomal
A;Reference number: A55454; MUID:95050610; PMID:7961765
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F;77-100/Domain: leucine-rich alpha-2-giroprotein repeat homology <LRR2>
F;101-124/Domain: leucine-rich alpha-2-giroprotein repeat homology <LRR2>
F;125-145/Domain: leucine-rich alpha-2-giroprotein repeat homology <LRR4>
F;146-169/Domain: leucine-rich alpha-2-giroprotein repeat homology <LRR4>
F;170-193/Domain: leucine-rich alpha-2-giroprotein repeat homology <LRR5>
F;196-216/Domain: leucine-rich alpha-2-giroprotein repeat homology <LRR5>
F;217-240/Domain: leucine-rich alpha-2-giroprotein repeat homology <LRR7>
F;247-264/Domain: leucine-rich alpha-2-giroprotein repeat homology <LRR8>
F;265-287/Domain: leucine-rich alpha-2-giroprotein repeat homology <LRR9>
F;265-287/Domain: leucine-rich alpha-2-giroprotein repeat homology <LRR9>
F;268-302/Domain: leucine-rich alpha-2-giroprotein repeat homology <LRR9>
F;268-302/Domain: leucine-rich alpha-2-giroprotein repeat homology 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 LAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAK 230
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                                                                                       221 PPSLTELHLDGNKITKIDASSLKGLNNLAKLGLSFNDISAVDNGSLANAPHLRELHLDNN 280
                                                                                                                                                          299 KLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEM 358
                                                                                                                                                                                                56 FPTREPRSHFFPFD----LFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNN 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 KIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 LTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRV 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 FMLEDEASGIIPYDPUPLISMCPYRCQCHLRVVQCSDLGLDKVPWDFPPDTTLLDLQNN 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Naitch, Y:; Sizuki, S. submitted to the EMBL Data Library, July 1990 A; Description: Wucleotide sequences of cDNAs encoding mouse PGI and PGII. A; Reference number: $20811 A; Accession: $20812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-354 <SCH>
A;Cross-references: GB:X53929; NID:953668; PIDN:CAA37876.1; PID:953669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N; Alternate names: proteoglycan II
                                                                                                                                                                                                                                                                                               359 QPATFRCVLSRMSVQLGNF 377
                                                                                                                                                                                                                                                                                                                                                                  341 QPSTFRCVYMRSAIQLGNY 359
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A;Molecule type: mRNA
A;Residues: 1-354 <NAI>
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Best Local Similarity
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C; Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan F:49-737Domain: proteoglycan amino-terminal homology <PAH>
F:49-73Domain: proteoglycan amino-terminal homology <PAH>
F:49-73Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:107-130/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:131-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:131-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:107-199/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:202-222/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:247-270/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F:247-270/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F:247-270/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F:247-285/Domain: leucine-rich alpha-2-glycoprotein repeat homology </ri>
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A;Title: Cloning and in situ hybridization of rabbit decorin in corneal tissues. A;Reference number: I47020, MUID:95122319; PMID:7822148
A;Accession: I47020
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-360 <ZHA>
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C;Date: 04-Sep-1997 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 NKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGL 238
                                                                                                                                                                                                                                                                                                      60 EPRSHFFFFDLFFMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEN 119
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60 EPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEN 119
                                                               EP-----MGPVCPFRCQCHLRVVQCSDLGLEKVPKDLPPDTALLDLQNNKITEIKDG 100
                                                                                                                                 120 DFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHE 179
                                                                                                                                                                    180 NKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGL 238
                                                                                                                                                                                                                                                                                                                                                                                                     PPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENN 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221 PPSLTELHLDGNKITKVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHLRELHLNNN 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KIKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEM 358
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F;309-360/Domain: proteoglycan carboxyl-terminal homology <PCH>
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C;Accession: A41748; B41748
R;Blochberger, T.C.; Vergnes, J.P.; Hempel, J.; Hassell, J.R.
J. Biol. Chem. 267, 347-352, 1992
A;Title: cDNA to chick lumican (corneal keratan sulfate proteoglycan) reveals homolog
A;Reference number: A41748; MUID:92112674; PMID:1370446
A;Accession: A41748
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N;Alternate names: 37K keratan sulfate-linked protein; corneal keratan sulfate proteo
C;Species: Bos primigenius taurus (cattle)
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A;Residues: 55-76 <BL2>
C;Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology
C;Keywords: glycoprotein; tandem repeat
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-343/Product: lumican #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Umican precursor - chicken
N;Alternate names: corneal keratan sulfate proteoglycan
C;Species: Gallus gallus (chicken)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 04-Sep-1998
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                                                                                                                                                                                                                                        291 REIHLENNKLKKIPSGLPELK--YLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISL 348
LENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVK 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 AELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKL 231
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                                                                                      PKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIH 294
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                                                                                                                                                                                                                                                                                                                               355 YWEMQPATFRCVLSRMSVQLGNF 377
                                                                                                                                                                                                                                                                                                                                                                 331 YWQIHPHTFRCVFGRSTIQLGNY 353
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A;Accession: B41748
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A; Residues: 1-343 <BL1>
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C.Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan C.Keywords: collagen blading; extracellular matrix; glycoprotein
C.Keywords: collagen blading; extracellular matrix; glycoprotein
E.1-30/Domain: slgnal sequence (fragment) # status predicted <SIG>
F;31-354/Product: decorin #status predicted <MAT>
F;31-364/Product: decorin #status predicted <MAT>
F;31-364/Domain: proteoglycan amino-terminal homology <PAH>
F;37-100/Domain: proteoglycan amino-terminal homology <ALRR2>
F;37-100/Domain: leucine-rich alpha-2-glycoprotein repeat homology <ALRR2>
F;101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <ALRR4>
F;101-134/Domain: leucine-rich alpha-2-glycoprotein repeat homology <ALRR5>
F;106-216/Domain: leucine-rich alpha-2-glycoprotein repeat homology <ALRR6>
F;21-240/Domain: leucine-rich alpha-2-glycoprotein repeat homology <ALRR8>
F;21-26-287/Domain: leucine-rich alpha-2-glycoprotein repeat homology <ALRR9>
F;265-287/Domain: leucine-rich alpha-2-glycoprotein repeat homology <ALRR9>
F;303-354/Domain: proteoglycan carboxyl-terminal homology <PCH>
F;303-354/Domain: proteoglycan carboxyl-terminal homology 
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Eur. J. Cell Biol. 59, 314-321, 1992
A;Title: Molecular characterization of vascular smooth muscle decorin: deduced core JA;Reference number: 160238; MUID:93154359; PMID:1493796
A;Reference number: 160238
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                                                                                                                                                                                                                                                                                                                                                                                                                            N.Alternate names: dermatan sulfate proteoglycan-II
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
C;Accession: S29145; 160238; S28517
R;Abramson, S.R; Woessen Jr. J.F.
Biochim. Biophys. Acta 1132, 225-227, 1992
A;Title: CDN Sequence for rat dermatan sulfate proteoglycan-II (decorin).
A;Reference number: S29145; MUID:93003331; PMID:1390895
116 IKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAEL 175
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                                                                                                                     60 EPRSHFFFFD----LFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 RIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVT-VFHIRIAEAKLISV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKATLVLF1LAQVSWAGPF---EQRGLFDFMLED-------31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-354 <ABR>
A;Cross-references: EMBL:212298; NID:957549; PIDN:CAA78170.1; PID:957550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X59859; NID:g56056; PIDN:CAA42519.1; PID:g56057 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 354;
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; Pred. No. 5.2e-54;
70; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                           |||:|||: | ||||: | ||||| | ::||||: | 353 | NPVRYWEIFPUTFRCVYVRSAIQLGNY 353
                                                                                                                                                                                                         351 NPVKYWEMQPATFRCVLSRMSVQLGNF 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 11-354 <RES>
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Best Local Similarity
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A; Molecule type: mRNA
A; Residues: 1-382 <RES>
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C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 24-Sep-1999
C;Accession: A46743; A35379
R;Funderburgh, J.L.; Funderburgh, M.L.; Brown, S.J.; Vergnes, J.P.; Hassell, J.R.; Mann, J. Biol. Chem. 266, 11874-11880, 1993.
A;Title: Sequence and structural implications of a bovine corneal keratan sulfate protect A;Reference number: A46743; MUID:93280153; PMID:8099356
A;Accession: A46743; MUID:93280153; PMID:8099356
A;Accession: A46743; MUID:93280153; PMID:8099356
A;Reference number: A46743; MUID:91809356; PIDN:AAA30608.1; PID:g163267
A;Resperimental source: cornea
R;Funderburgh, J.L.; Conrad, G.W.
J. Biol. Chem. 265, 8297-8303, 1990
A;Title: Isoforms of corneal keratan sulfate proteoglycan.
A;Reference number: A35379; MUID:90243714; PMID:2139877
A;Residues: 19-36 <FUZ>
A;Residues: 19-36 <FUZ>
A;Residues: 19-36 <FUZ>
A;Resperimental source: cornea
C;Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology
C;Reywords: glycoprotein; tandem repeat
E;1-18/Domain: signal sequence #status predicted <AMAT>
F;19-342/Product: lumican #status predicted <AMAT>
F;92,131,164,256/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C.Species: Rattus norvegicus (Norway rat)
C.Accession: $52284
R.Krull, N.B.
submitted to the EMBL Data Library, January 1995
A.Recession: $52284
A.Accession: $52284
A.Accession: $52284
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-338
A.Rolecule type: mRNA
A.Residues: 1-338
A.Coss-references: EMBL:X84039; NID:g643023; PIDN:CAA588658.1; PID:g643024
C.Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 FPFDLF----PMCPFGCQC---YSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 NDFKGLTSLYGLILNNNKL--TKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAFENVIDLQWLILDHNLLENSKIKGKVFSKLKQLKKLHINYNNLTESVGPLPKSLVDLQ 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 IHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVP 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 KGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDI-ENGSLANIPRVREIH 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 LENNKLKKIPSGLPELK--YLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNP 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 LSYNKLKSIPTVNENLENYYLEV----NELEKFDVKSFCKILGPLSYSKIKHLRLDGNH 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 SGLPVSLLTLYLDNNKISNIPDEYFKRFSALQYLKLSHNELADSGVPGNSFNVSSLLELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.3%; Score 384; DB 2; Length 342
32.2%; Pred. No. 6.3e-19;
.ive 68; Mismatches 123; Indels
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32.2%; Pred. No. 1.6e-18;
Live 67; Mismatches 123; Indels
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Matches 99; Conservative
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R;Bengtsson, E.; Neame, P.J.; Heinegard, D.; Sommarin, Y.
J. Biol. Chem. 270, 25639-25644, 1995
A;Title: The primary structure of a basic leucine-rich repeat protein, PRELP, found i. A;Reference number: I39068; MUID:96029653; PMID:7592739
A;Accession: I39068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proline- arginine-rich end leucine-rich repeat protein PRELP precursor - human
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C;Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology
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C;Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 24-Sep-1999
69 DLFPMCPFGCQC---YSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLT 125
                                                                                                                                                     .26 SLYGLILNNNKL--TKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVK 183
                                                                                                                                                                                                                         91 DLOWLILDHNELENSKIKGKVFSKLKQLKKLHINYNNLTESVGPLPKSLQDLQLANNKIS 150
                                                                                                                                                                                                                                                                                                                                                          301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 SIPTVNENLENYYLEV----NKLEKFDVKSFCKILGPLSYSKIKHLRLDGNPLTQSSLP 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:U29089; NID:g886135; PIDN:AAC50230.1; PID:g886136
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 HIRIAEAKLISVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITD--IE 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 DDDDEDNSLFPTREPRSHFFPFDLFPMCPFGCQC---YSRVVHCSDLGLTSVPTNIPFDT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 RMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 HYLYLONNFITELPVESFONATGLRWINLDNNRIRKIDQRVLEKLPGLVFLYMEKNOLEE 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 IPLNLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVF 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225 QLNLAHNILRKMPPRVPTAIHQLYLDSNKIETIPNGYFKSFPNLAFIRLNYNKLTDRGLP 284
                                                                        32 ELSPNCAPECNCPHSYPTAMYCDDLKLKSVPM-VPPGIKYLYLRNNQIDHIDEKAFENVT
                                                                                                                                                                                                                                                                                                          .84 KIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGLPPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 LELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDI-ENGSLANIPRVREIHLENNKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 LTLYLDNNKITNIPDEYFNRFTGLQYLRLSHNELADSGVPGNSFNISSLLELDLSYNKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302 KIPSGLPELK--YLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQ
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Matches 90; Conservative
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Query Match
Best Local
A; Accession:
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fibromodulin - chicken
Cibromodulin - chicken
Cibromodulin - chicken
Cibate: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 24-Sep-1999
C:Accession: S71876
Fibruminskaya, M.V.; Birk, D.E.
Biochem. J. 317, 785-789, 1996
A;Title: Differential expression of fibromodulin mRNA associated with tendon fibril grow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.71tle: Identification of the keratan sulfate attachment sites on bovine fibromodulin. A.Reference number: A23663; MUID:91056119; PMID:2243109
A.Reference number: A23663; MUID:91056119; PMID:2243109
A.Roontents: annotation; keratan sulfate attachment
C:Comment: Reratan sulfate can be covalently attached to N-acetylglucosamine at the aspa C:Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology
C:Keywords: cartilage; chondroitin sulfate proteoglycan; collagen binding; connective tip: F:1-18/Domain: signal sequence #status predicted SIG>
F:19-375/Product: fibromodulin #status experimental <AMAT>
F:38,42,45,47,50,53,62,64/Binding site: sulfate (Tyr) (covalent) #status predicted
F:126,165,200,290/Binding site: carbohydrate (Asn) (covalent) #status experimental
        fibromodulin precursor - bovine

N.Alternate names: 59K collagen-binding matrix protein

C;Species: Bos primigenius taurus (cattle)

C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 24-Sep-1999

C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 24-Sep-1999

C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 24-Sep-1999

R;Oldberg, A: Antonsson, P.; Lindblom, K.; Heinegard, D.

EMBO J. 8, 2601-2604, 1989

EMBO J. 8, 2601-2604, 1989

A;Title: A collagen-binding 59-kd protein (fibromodulin) is structurally related to the A;Reference number: S05390; MUID:90060020; PMID:2531085
                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-375 COLD>
A;Toss-references: GB:X16485; EMBL:X16305; NID:g353; PIDN:CAA34503.1; PID:g354
A;Accession: S26942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 LPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRI 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 LPRSLRELHLDHNQISRVPNNALEGLENLTALYLHHNEIQEVG---SSMKGLRSLILLDL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLA- 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 SYNHLKKVPDGLPSALEQLYLEHNNVFSVPDSYFRGSPKLLYVRLSHNSLT---NNGLAS 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---NIPRVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 287 NTFNSSSLELDLSYNQLQKIP---PVSTNLENLYLQGNRINEFSISSFCTVVDVMNFSK 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 ----PTREPRSHFFPFDLFPMCPFGCQC---YSRVVHCSDLGLTSVPTNIPFDTRMLDLQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 NNKIKEIKENDFKGLTSLYGLILNNNKLT--KIHPKAFLTTKKLRRLYLSHNQLSEIPLN 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 ILLLAGLCSLSWAQYEEDSHWWFQ--FLRNQQSTYDDPYDPYPYEPYEPYPTGEEGPAYA 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 342.5; DB 2; Length 3:
; Pred. No. 4.8e-16;
66; Mismatches 158; Indels
                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 90-105;190-199;274-281 <0L2>
R;Plaas, A.H.K.; Neame, P.J.; Nivens, C.M.; Reiss, L.
J. Biol. Chem. 265, 20634-20640, 1990
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27.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               343 YSAISLFNNPVK 354
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NATIEFTATE names: Slit protein homolog (Species: Rattus norregicus (Norway rat) (C)Species: Rattus norregicus (Norway rat) (C)Species: Rattus norregicus (Norway rat) (C)Accession: T13953 (C)Accessio
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C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotei
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                                                                                                     A;Status: preliminary
A;Molecule type: mRnA
A;Residues: 1-380 AUNRA
A;Residues: 1-380 AUNRA
A;Cross-references: EMBL:U34977; NID:g1098905; PIDN:AAC60016.1; PID:g1098906
C;Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 CPFGCQC---YSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 CPQECDCPPNFSSAMYCDTRNLRYLPF-VPTRMKYVYFONNOITAIOEGAFDNATELEWL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 ILNNNKLT--KIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKD 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 ALHNNQISSEKMGKRVFAKLKNLERLYMNNNNLTKMPSPLPRSLRELHLSYNQISKVPSN 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 DYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLA----NIPRVREIHLENNKLKKI 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.7%; Score 333.5; DB 2; Length 380; 30.1%; Pred. No. 2e-15; ive 61; Mismatches 134; Indels 21
A; Reference number: S71876; MUID: 96332470; PMID: 8760363
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Best Local Similarity
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Oy 223 230	fibromodulin precursor – human N;Alternate names: 59K collagen-binding matrix protein
Db 209 TLRLHSNHLYCDCHLAWLSDWLRQRRTIGQFTLCMAPVHLRGFSVADVQKKEYVCPGPHS 268	C;Species: Homo sapiens (man)
Qy 231	C, Accession: S55275; S35710; S32752; S41925
Db 269 EAPACNANSLSCPSACSCSNNIVDCRGKGLTEIPANLPEGIVEIRLEQNSIKSIPAGAFI 328	K;Hildebrand, A.; Komaris, M.; Kasmussen, L.M.; Heinegard, D.; Iwardzik, D.K. Biochem. J. 302, 527-534, 1994
Oy 262 RYKELORLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSGLPE-LKYLOIIFLHS 320	A;Title: Interaction of the small interstitial proteoglycans biglycan, decorin and fi A:Reference number: S5275; MUID:94379985; PMID:8093006
329 OYKKLKRIDISKNOISDIAPDAFOGLKSLTSLVLYGNKITEIPKGLPDGLVSLOLLLLNA 388	A; Accession: S55275 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
NSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVK 354	A; Molecule type: mRNA A; Residues: 1-376 <hi2></hi2>
389 NKTNCIRVNTFODICOLINIARY OF 416	A;Cross-references: EMBL:X7546; NID:g453156; PIDN:CAA53233.1; PID:g453157 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993
	R;Antonsson, P.; Heinegard, D.; Oldberg, A. Riochim Biophys, Arta 1174, 204-206, 1993
RESULT 18	A)Title: Structure and deduced amino acid sequence of the human fibromodulin gene.
	A/Accession: S35710
	A;Molecule type: DNA A;Residues: 1-3,′T′,5-86,′P′,88-209,′N′,211-225,′Y′,227-343,′O′,345-354,′M′,356-362,′
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2002	A; Cross-references: EMBL: X72913; NID: 9297090; PIDN: CAA51418.1; PID: 9297091
	C; connection returns arrange can be covared a accorded to acceptation and a connection and a connection are a connections.
GGF-like motifs	A;Cross-references: GDB:228979; OMIM:600245
Z14126; MUID:98360089; PMID:9693030	A;Map position: 1q32.1-1q32.1 A:Introns: 326/2
sliminary; translated from GB/EMBL/DDBJ	C; Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology
	C;Keywords: cartilage; cnondroltin sulfate proteoglycan; collagen binding; connective F;1-18/Domain: signal sequence #status predicted <sig></sig>
rrences: EMBL:AB011530; NID:g3449289; PIDN:BAA32460.1; PID:g3449290 al source: strain Spraque-Dawley; brain	F;19-376/Product: fibromodulin #status predicted <mat> F;38,39,42,45,47,50,53,55,63,65/Binding site: sulfate (Tyr) (covalent) #status predic</mat>
	F;127,166,201,291/Binding site: carbohydrate (Asn) (covalent) #status predicted
C; Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r	Query Match 16.0%; Score 318; DB 2; Length 376;
16.2%; Score 323;	imitality 20.1%; Fied. NO. ; Conservative 65; Mismate
best Local Similarity 25.0%; Pred. No. 5.4e-14; Matches 98; Conservative 64; Mismatches 116; Indels 114; Gaps 10;	Qy 63 SHFFPFDLFPM
QY 74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDL 108	Db 37 TYYDPYDPYETYEPYPYGVDEGPAYTYGSPSPPDPRDCPQECDCPPNFLTAMYCDNRN 96
	OV 92 LTSVPTNTPPDTRMLDLONNKTKEIKENDFKGLTSLVGLILANNKLTKIHPKAFLTTK 149
109 QNNKIKEIKENDEKGLISLYGGLINNNKLIKIHPKAFLITIKKLKRINGLSELP	9/ LKYLPF-VPSKMKYVYFQNNQITSIQEGVFDNATGLLWIALHGNQITSDKVGKKVFSKLR
	KERREYESHNOESEIPENEPRSEABELKIHENKYRKIQKUTFKGMNALHVEMSANPEDNN ZU              : :    :      : : : : : :
QY 166 LNLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIE 212	Db 156 HLERLYLDHNNLTRMPGPLPRSLRELHLDHNQISRVPNNALEGLENLTALYLQHDEIQEV 215
Db 401 FQDLQNLSLLSLYDNKIQSLAKGTFTSLRAIQTLHLAQNPFICDCNLKWLADFLRTNPIE 460	PTLL.
Qy 213 -PGA 223	Db 216 GSSMRGLRSLILLDLSYNHLRKVPDGLPSALEQLYMEHNNVYTVPDSYFRGAPKLLY 272
Db 461 TTGARCASPRILANKRIGQIKSKKFRCSAKEQYFIPGTEDYHLNSECTSDVACPHKCRCE 520	QY 269 LGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIA 324
Qy 224IRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELED-FKRYKELQRLGLGNKITDI 279	DD 273 VRLSHNSLTNNGLASNIFNSSSLLELDLSYNQLQKIPPVNTNLENLYLQGNRIN 326
Db 521 ASVVECSGLKLSKIPERIPQSTTELRLNNNEISILEATGLFKKLSHLKKINLSNNKVSEI 580	OY 325 RVGVNDFCPTVPKMKKSLYSAISLFNNPVK 354
SLANIPRVREIHLEN	DD 327 EFSISSFCTUVDUVNFSKLQVVRLDGNEIK 356
Db 581 EDGTFECATSVSELHLTANQLESVRSGMFRGLDGLRTLMLRNNRISCIHNDSFIGLRNVR 640	
Qy 339 KKSLYSAISLFNNP 352	RESULT 20 B36665
	ly (Drosophila melanogaster)
	C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002 C;Accession: B36665
RESULT 19 S55275	R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S. Genes Dev. 4, 2169-2187, 1990

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Signoises Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Date: 30-Apr.1991 #sequence_revision 30-Apr.1991 #text_change 02-Aug-2002
C; Accession: A36665; A31640; S13523
R; Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A; Title: slit: an extracellular protein necessary for development of midline glia and A; Reference number: A36665
A; Accession: A36665
A; Accession: A36665
A; Reference number: A36665
A; Residues: 1-1480 cROT>
A; Residues: 1-1480 cROT>
A; Residues: 1-1480 cROT>
A; Coll 55, 1047-1059, 1988
A; Reference number: A31640
A; Title: slit: An EGF-homologous locus of D. melanogaster involved in the development A; Reference number: A31640
A; Molecule type: DNA
A; Residues: B81-1182, G', 1185-1404, GT', 1463-1464, YHA' cRO2>
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C; Generics: Conservation: A31640
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A; Cross-references: GB:M23343; NID:g340939; PID:g514357
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A;Cross-references: FlyBase:FBgn0003425
A;Cross-references: FlyBase:FBgn0003425
A;Cross-references: FlyBase:FBgn0003425
A;Introns: 1351/2
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F;149-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR3>
F;137-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR3>
F;137-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR3>
F;28-272/Domain: protecoglycan carboxyl-terminal homology cRR3>
F;28-272/Domain: protecoglycan carboxyl-terminal homology cRR3>
F;28-372/Domain: protecoglycan amino-terminal homology cRR8>
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F;377-257/Domain: protecoglycan amino-terminal homology cRR3>
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F;67-657/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLR10>
F;67-697/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLR10>
F;61-695/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLR10>
F;61-695/Domain: leucine-rich alpha-2-glycoprote
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 316; DB 2; Length 1480;
Pred. No. 1.8e-13;
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Matches 9
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C; Superfamily: fruit fly slit protein: BGF homology; leucine-rich alpha-2-glycoprotein repeat homology chall.
F; 66-91/Domain: proteoglycan amino-terminal homology, PAHI>
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F; 101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR2>
F; 149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR4>
F; 173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR5>
F; 173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR5>
F; 228-272/Domain: proteoglycan carboxyl-terminal homology cPR12>
F; 238-346/Domain: proteoglycan amino-terminal homology cPR12>
F; 337-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR6>
F; 347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR8>
F; 347-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR9>
F; 348-40/Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR9>
F; 450-494/Domain: proteoglycan carboxyl-terminal homology cPCS2>
F; 537-537/Domain: proteoglycan carboxyl-terminal homology CRR9>
F; 515-537/Domain: proteoglycan carboxyl-terminal homology CRR9>
                                             S
A;Title: slit: an extracellular protein necessary for development of midline glia and A;Reference number: A36665; MUID:91099665; PMID:2176636
A;Accession: B36665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----RMLDLQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 CPRVCSCTGLNVDCSHRGLTSVPRKISADVERLELQGNNLTVIYETDFQRLTKLRMLQLT 132
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; Pred. No. 1.8e-13;
66; Mismatches 123; Indels 104; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 KSLAELRI ---HENKVKKIQKDTFKGMNALHVLEMSANPL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :||::| : : | | : | : | | SLLSLYDNNIQ--SLANGTFDAMKSMKTVHL 449
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25.1%;
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                                                                                                                                                                                                                                                                                                                         A; Residues: 1-1469 <ROT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                       A;Status: preliminary A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: FlyBase:sli
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RESULT 21

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C,Accession: T42626
R;Holmes, G.P.: Negus, K.; Burridge, L.; Raman, S.; Algar, E.; Yamada, T.; Little, M. Mech. Dev. 79, 57-72, 1998
A;Title: Distinct but overlapping expression patterns of two vertebrate slit homologs A;Reference number: 222177; MUID:99279238; PMID:10349621
A;Accession: T42626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: A53860
R;Neame, P.J.; Sommarin, Y.; Boynton, R.E.; Heinegard, D.
J. Biol. Chem. 269, 21547-2154, 1994
A;Title: The structure of a 38-kpa leucine-rich protein (chondroadherin) isolated fro A;Reference number: A53860; MUID:94342341; PMID:8063792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:U08018; NID:g470671; PIDN:AAA21330.1; PID:g470672
C;Superfamily: Leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan carbox
C;Keywords: disulfide bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: Slit2
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotei
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: 38K leucine-rich protein
C;Species: Bos primigenius taurus (cattle)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N;Alternate names: neurogenic extracellular slit protein
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 16-Aug-2002
FYLDRNQLSSYPSAALSKLRVVEELKLSHNPLKSIPDNAFQSFGRY--LETLWLDNTNLE 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 LQHCQIREVAAGAFRGLKQLIYLYLSHNDIRVLRAGAFDDLTELTYLYLYLDHNKVTELPRG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 LPKSLAE----LRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFH 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 IRIAEAKLTSVPKGLPPTLL---ELHLDYNKISTV---ELEDFKRYKELQRLGLGNNKIT 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                secreted leucine-rich repeat-containing protein SLIT2 - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.8%; Score 294; DB 2; Length 361; 27.5%; Pred. No. 9.2e-13; ive 58; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;300-346/Domain: proteoglycan carboxyl-terminal homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 CPFGCQCYSRVVH--CSDLGLTSVPTNIPFDTRMLDLQNN-------
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                                                                                                                                                                                                                                                                                                                                                                                  chondroadherin precursor - bovine
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                                                                                                            361 ATFRCVLSRMSV 372
                                                                                                                                                                                     330 AE----LSSLSI 337
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A; Residues: 1-1025 <HOL>
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A; Residues: 1-361 <NEA>
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A; Status: preliminary
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A; Molecule type: mRNA
A; Residues: 1-1091 (S017)
A; Cross-references: GB:D78572; NID:91545806; PIDN:BAA11416.1; PID:91545807
A; Cross-references: GB:D78572; NID:91545806; PIDN:BAA11416.1; PID:91545807
C; Superfamily: leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan amino-ter
F; 36-61/Domain: proteoglycan amino-terminal homology (ADRA)
F; 71-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology (ALRR2)
F; 71-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology (ALRR2)
F; 11-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology (ALRR5)
F; 191-213/Domain: leucine-rich alpha-2-glycoprotein repeat homology (ALR85)
F; 191-213/Domain: leucine-rich alpha-2-glycoprotein repeat homology (ALR87)
F; 238-26/Domain: leucine-rich alpha-2-glycoprotein repeat homology (ALR10)
F; 262-285/Domain: leucine-rich alpha-2-glycoprotein repeat homology (ALR10)
F; 338-36/Domain: leucine-rich alpha-2-glycoprotein repeat homology (ALR10)
F; 338-381/Domain: leucine-rich alpha-2-glycoprotein repeat homology (ALR12)
F; 385-408/Domain: leucine-rich alpha-2-glycoprotein repeat homology (ALR12)
F; 386-408/Domain: leucine-rich alpha-2-glycoprotein repeat homology (ALR12)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gibal cell membrane glycoprotein LIG-1 precursor - mouse
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: Musculus ASB332
Sizuki, Y.; Sato, N.; Tohyama, M.; Wanaka, A.; Takagi, T.
J. Biol. Chem. 271, 22522-22527, 1996
A;Title: CDNA cloning of a novel membrane glycoprotein that is expressed specifically A;Reference number: A58532; MUID:96394313; PMID:8798419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                          LKOLTILVLYGNKIKDLPSGVFKGLGSLRLLLLNANEISCIRKDAF-----RDLHSL 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEI----PLNLPKSLAELRIHENKVKKIQKDTF 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 SNELTAI-PSLGTASIGVVSLFLQHNKILSVDGSQLKSYLSLEVLDLSSNNITEIRSSCF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 KGMNALHVLEMSANPLDNNG1---EPGAFEGV--TVFHIRIAEAKLTSVP-KGLP-PTLL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 P--NGLRIRELN---LASNRISILESGAFDGLSRSLLTLRLSKNRITQLPVKAFKLPRLT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 ELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKI 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 QLDLNRNRIRLIEGLTFQGLDSLEVLRLQRNNISRLTDGAFWGLSKMHVLHLEYNSLVEV 276
                                                                                                            253 PYTRCQSPSQLKGQNVADLHDQEFKCSGLTEHAPMECGAENSCPHPCRCADGI----VDC 308
                                                                                                                                                                                         227 AEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLAN 286
                                                                                                                                                                                                                                                                 309 REKSLTSVPVTLPDDTTDVRLEQNFITELPPKSFSSFRRLRRIDLSNNNISRIAHDALSG 368
                                                                                                                                                                                                                                                                                                                                              287 IPRVREIHLENNKLKKIPSGL-PELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLY-- 343
                                        ---FEGVTVFHIRI 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 296; DB 2; Length 1091;
; Pred. No. 2.8e-12;
64; Mismatches 124; Indels 30;
                                        -DNNGIEPGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLLSLYDNNIQ--SLANGTFDAMKSMKTVHL 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 SAISLFNNPVKYWEMQPATFRCVLSRMSVQL 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.9%;
30.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421
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                                                                                                            pp
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Query Match 14.2%; Score 282.5; DB 2; Length 1025; Best Local Similarity 22.8%; Pred. No. 2.2e-11; Matches 89; Conservative 65; Mismatches 128; Indels 109; Gaps 9;	Qy 305 -SGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSA 345
CYSRVVHCSDLGLTSVPTNTPFDT	Db 454 FQGLGHLEYLLLSYNQLTTLSAEVLGPLQRAFWLDISHNHLETLAEGLFSSLGRVRY 510
:	346 ISLFNNPVKYWEMQPATFR
109 QNNKIKEIKENDFKGLTSLYGLILUNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNL 1	110
LRSNRISCVGNDS 1	RESULT 26 JC7763
DD 122 FIGLGSVRLESLYDNQTITVAPGAFDXLHSLSTLNLLANPFNCNCHLAWLGEWLRRKRIV 181	neuronal leuchne-rich repeat protein-3 - rat C.Species: Rattus norvegicus (Norway rat) C.Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
Qy 210GIEPGAFBGVŢVFHIRIAEAKL 231	C:Accession: JC/7/83 R:Fukamachi, K.; Matsuoka, Y.; Kitanaka, C.; Kuchino, Y.; Tsuda, H. Biochem. Biophys. Res. Commun. 287, 257-263, 2001 A.Title: Rat neuronal leucine-rich repeat profein-3: Cloning and regulation of the general and professions.
7	27763; PMID:11549284
292 EIHLENNKLKKI-PSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAIS 3	A;Molecule type: mkNA A;Residues: 1-707 <fuka a="" a;cross-references:="" c;comment:="" fam<="" fhis="" gb:af291437="" leucine-rich="" member="" neuronal="" new="" of="" protein="" protein,="" repeat="" td="" the=""></fuka>
OD 348 LENNPVKYWEMOPATERC 365  Qy 348 LENNPVKYWEMOPATERC 365	in protein-protein interaction and functions as a cell adhesion molecule or soluble 1 C;Genetics: A;Gene: nlrr-3 A;Gene: nlrr-3
Db 352 IGANPLYCDCUMQWLSDWYKSEYKEPGIARC 382	adhesion
RESULT 25	Query Match 13.4%; Score 266; DB 2; Length 707; Best Local Similarity 24.1%; Pred. No. 1.8e-10; Matches 92; Conservative 70; Mismatches 118; Indels 102; Gaps 16;
insulin-like growth factor-binding protein acid labile chain precursor - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jul-2000	QY 74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIK 117
R.Dai, J.; Baxter, R.C. Biochem. Biophys. Res. Commun. 188, 304-309, 1992 A;Title: Molecular cloning of the acid-labile subunit of the rat insulin-like growth fa	OY 118BDDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLS 157 :  :           :       :  :
A;Keterence number: JC1282; MUID:93038676; PMID:1384485 A;Accession: JC1282 A:Molecule trons: mpxx	QY 158 HNOLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLD 207
A; Residues: 1-603 CDAI> A; Residues: 1-603 CDAI> A; Cross-references: GB:S46785; NID:g258002; PIDN:AAB23770.2; PID:g5705934	Db 149 HNLLSAISPGAFVGLHNLLRLHLNSNRLQMINSKWFEALPNLEILMLGDNPILRIKD 205
A; Experimental source: liver A; Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205 (S; Superfamily: leucine-rich alpha-2-glycoprotein repeat homology	OY 208 NN
F;1-2//Domain: Signal Sequence #Status predicted <sig> F;28-603/Product: insulin-like growth factor binding protein, acid labile chain #status F;267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lrr></lrr></sig>	OY 242 LLELHLDYNKISTVELEDFKRYKELQRLGLGN-NKITDIENGSLANIPRVREIHLENN-K 299  Dh 262 IKFLDINKNDFNRTEDFORESMITHIKFLGINNADERIVETNETNGFNADERIOGYERANMANDE 221
Query Match 13.7%; Score 272; DB 2; Length 603; Best Local Similarity 28.2%; Pred. No. 5.7e-11; Matches 90; Conservative 57; Mismatches 108; Indels 64; Gaps 12;	300 LKKI-PSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSALSLFNNPVK
QY 102 DTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQL 161 :               : :	Db 322 LSYIHPNAFFRLPKLESLMLNSNALSAL-YHGTIESLPNLKEISIHSNPIRCDCV 375 OY 355 -YWEMQPATFRCV 366
	Db 376 IRWINMNKTNIREMEPDSLFCV 397
Db 279 AGLMEDTFPGLLGLHVLRLAHNAIASLRPRTFKDLHFLEELQLGHNRIRQLGERTFEGLG 338	RESULT 27
Qy 195 ALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHL 247         :-   :   :	insulin-like growth factor binding complex acid labile chain - mouse C; Species: Mus musculus (house mouse) C; Date: 23-Mar-1997 #sequence_revision 09-May-1997 #text_change 05-Nov-1999
OY 248 DYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIP 304 ::::	C:Accession: JC6128 R;Boisclair, Y.R.; Seto, D.; Hsieh, S.; Hurst, K.R.; Ooi, G.T. Proc. Natl. Acad. Sci. U.S.A. 93, 10028-10033, 1996 A;Title: Organization and chromosomal localization of the gene encoding the mouse aci

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and regulation of the ge
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ion molecule or soluble l
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SLYSA----- 345
|:|:
GLFSSLGRVRY 510
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                                                                                                                                                                                                                                                                                                                                                                                                                   TTKKLRRLYLS 157
|: ||::
SLSNLQELYVN 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTSVPKGLPPT 241
:: | :
)VALQKAV--N 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /REIHLENN-K 299
:|:| | | ;
LRKIEATNNPR 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nge 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LFNNPVK---- 354
::||::
IHSNPIRCDCV 375
                                                                                                                                                                                                                                                                                                                                                                           NKIKEIK--- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SANPL----D 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDNPILRIKD 205
                                                                                                                                                                                                                                                                                                                                                      s 102; Gaps
                                                                                                                                                                                                                                                                                                                                                                                           | | |:
NNIARIEHST 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - mouse
                                                                                                                                                                  uda, H.
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A;Reference number: JC6128; MUID:96413591; PMID:8816745	Db 311 AFHGLNELYAVNLTDVGLAIINPDTFVGNKKLRMLTISGNDLSVMSSIHYLLKSSSIEEL 370
A;Accession: JC6128 A;Molecule type: DNA	Qy 176 RIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVF-HIRIAEAKLTSV 234
3 <boi> ss: GB:U66900; NID:g1621612; PIDN:AAB17270.1; PID:g1621613</boi>	Db 371 DFSRNNLMELNPKAFSHLSNVYZINLSQNSLKKLPEKAFEKVTLLEELDLSYNSLTEL 428
C:Comment: Ynis protein is a serum protein and it is of the ternary complex in the physicenetics: A:Genetics: A:Wap position: 17	QY 235 PKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGUNKITDIENGSLANIPRVRE 292  : :               :     :   :     :     :
Ouery Match Best Local Similarity 27.6%; Pred. No. 1.7e-10; Matches 88; Conservative 64; Mismatches 103; Indels 64; Gaps 12;	QY 293 IHLENNKLKKI-PSGLPELKYLQIIELHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNN 351 ::::
QY 102 DTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQL 161 :	Qy 352 P 352 Db 540 P 540
QY 162 SEIPLNLPKSLAELRIHENKVKKIQKDTFKGMN 194 : :         :	RESULT 29 JG0193
QY 195 ALHVLEMSANPLDNNGIEPGAPEGYTVFHIRIAEAKLTSVPKGLPPTILLELHL 247	G protein-coupled receptor FEX - mouse C;Species: Mus musculus (house mouse) C;Date: 23-Unl-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000 C;Accession: JG0193
QY 248 DYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIP 304 :::::	K; Hermey, G.; Methner, A.; Schaller, H.C.; Hermans-Borgmeyer, L. Blochem. Blophys. Res. Commun. 254, 273-279, 1920 A; Title: Identification of a novel seven-transmembrane receptor with homology to glyc. A; Reference number: JG0193; MUID:9912127; PMID:9920770
QY 305 -SGLPELKYLQIIFLHSNSIARVGVNDFCPTVPRMKKSLYSA 345	A.Accession: JG0193 A.Status: preliminarry A.Wolecule type: mRNA A.Residues: 1-907 <her></her>
Qy 346 ISLENNPVKYWEMOPATER 364 ::                Db 511 LNLRNNSLQTFVPQPGLER 529	Query Match 13.1%; Score 261.5; DB 2; Length 907; Best Local Similarity 21.8%; Pred. No. 5e-10; Matches 99; Conservative 68; Mismatches 127; Indels 161; Gaps 14;
RESULT 28 T13174	OY 69 DLFPM-CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLD
<pre>gpl50 protein - fruit fly (Drosophila melanogaster) C.Species: Drosophila melanogaster C.Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000 C.Accession: T13174</pre>	OY 108
R.Tian, S.S.; Zinn, K. J. Biol. Chem. 269, 28478-28486, 1994 A.Title: An adhesion molecule-like protein that interacts with and is a substrate for a A; Reference number: Z17630; MUID:95050638; PMID:7961789	QY 135 NKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLABLR
A.Accession: T13174 A.Accession: T13174 A.Status: preliminary, translated from GB/EMBL/DDBJ A.Molecule type: mRNA A.Residues: 1-1051 <tia></tia>	OY 177IHENKVKKIQKDTFKGMNALHVLEMSANPLDNN 209 
A:Cross-references: EMBL:U15220; NID:g595859; PID:g595860; PIDN:AAA61796.1 A:Experimental source: strain Oregon R C:Genetics: A:Cross-references: FlyBase:FBgn0013272	Qy 210 GI 223 
A;Map position: 2  Query Match  Best Local Similarity 27.1%; Pred. No. 3.5e-10;  Matches 98: Conservative 51: Mismatches 146: Indels 66: Gaps 12:	QY 224IRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNK 275 :                       : :     :   :
EDTDDDDDDDDDDDEDNSLFPTREPRSHFFPFDLFPMCPFGCQCYSRVVH 86	Qy 276 ITDIENGSLANIPRVREIHLENNKLKKI-PSGLPELKYLQIIFLHSNSIARVGVNDF 331   : : : : :   :
203 EGLEDDEDERDANDOLLIDDEQVYFSELVY 87 CSDLGLTSVPTNIPF-               251 CSRLDMGIQKFGSDITDLVVTNVGPKYPILI	QY 332 CPTVPKMKKSLYSAISLFNNP-VKYWEMQPATFRC 365 
OY 120 DFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAEL 175 	RESULT 30 T19939

hypothetical protein C44H4.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 C;Accession: T1939	do Oy
R.Smye, R. submitted to the EMBL Data Library, August 1996	qa :
A. Accession: T19939 A. Stetutus: prefilminary; translated from GB/EMBL/DDBJ	da —
A;Residues: 1-680 <wil> A;Cross-references: EMBL: Z79598; PIDN: CAB01865.1; GSPDB:GN00028; CESP: C44H4.3 A;Experimental source: clone C44H4</wil>	QY
A.Gene: CESP:C44H4.3 A.Map position: X A:Introns: 26/3; 74/3; 122/3; 216/3; 364/3; 589/3	RES
Query Match Best Local Similarity 29.1%; Pred. No. 4e-10; Matches 81; Conservative 49; Mismatches 119; Indels 29; Gaps 10;	10000 10000
0y 74 CPFGCQCYSRVVHCSDL-GLTSVPTNIPFDTRMLDLQNNKIKEIKEN 119	R;v A;d
QY 120 DFKGLTSLYGLILUNNKLTKIHPKAFLTTKK-LRRLYLSHNQLSEIPLNLPKSLAELRIH 178 	
QY 179 ENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLT 232 Db 135 NILSLKCNKIENITTKAFVNWTSLIDVNLGCNQICSMAADTFANVKMSLQNLILDNNCWT 194	
QY 233 SVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRIGGNNKITDIENGSLANIPR 289	# # # # # # # #
QY 290 VREIHLENNKLKKIPSG-LPELKYLQIIFLHSNSIARV 326 :::      ::      ::	F F F F F
RESULT 31 T19938	
<pre>hypothetical protein C44H4.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 C;Accession: T19938</pre>	QQ Oy
k;Smye, K. submitted to the EMBL Data Library, August 1996 A;Reference number: Z19200	δy
A;Accession: T19938 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA	a ò
A; Residues: 1-738 <wil> A; Cross-references: EMBL: 279598; PIDN: CAB01864.1; GSPDB: GN00028; CESP: C44H4.2 A; Experimental source: clone C44H4</wil>	. ପୁପ 
C.Genetics: A;Gene: CESP:C444.2 A:Man nocition: Y	O.Y
A;Introns: 30/3; 89/3; 125/3; 168/1; 327/3; 453/3; 524/3; 612/2; 680/2	an AO
Query Match 13.1%; Score 260.5; DB 2; Length 738; Best Local Similarity 25.9%; Pred. No. 4.5e-10; Matches 75; Conservative 62; Mismatches 110; Indels 43; Gaps 8;	ੇ <u>ਹ</u>
106 LDLQNNKIKEIKEND-FKGLTSLYGLILNNNKLTKIHPKAFLTTK-KLRRLYLSHNQLS	ζ, dg
Db 104 LDLSNNSIVEIQEQEIFFNINKLYDINLGSNKIFSIHTSTFQNVKNSIQTINLGHNNMTA 163 Qy 164 IPLNLPKSLAELRIHENKVKKIOKDFFKGNNALHVIFMSANDLINNKTFPGAFFGYP 220	Qy
:       :   :   :   :   :   :   :   :	q <sub>Q</sub>

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Accession: JE0176
McDonald, T.: Wang, R.; Bailey, W.; Xie, G.; Chen, F.; Caskey, C.T.; Liu, Q. iochem. Biophys. Res. Commun. 247, 266-270, 1998
Tritle: Identification and cloning of an orphan G protein-coupled receptor of the gl. Reference number: JE0176; MUID:98308104; PMID:9642114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecule type: mRNA
Residues: 1-907 cAMCD>
Cross-references: GBL>
Comment: This protein is a receptor for a novel class of glycoprotein ligands.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Homo sapiens (man).
Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 21-Jul-2000
164 VPSSAIRGLKQLQSLHLHKNRIEQLDALNFLNLPVLNLLNLAGNQI---HELNRQAFLNV- 220
                                                      221 VFHIRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIE 280
                                                                                                            ------PSLRYLYLSGNKITKLTAYQFQTFEQLEMLDLTNNEIGAIP 261
                                                                                                                                                                         281 NGSLANIPRVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIARV--GVNDFCPTVPKM 338
                                                                                                                                                                                                       94 ELRLAGNALTYIPKGAFTGLYSLKVLMLQNNQLRHVPTEALQNLRSLQSLRLDANHISYV 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----KSLA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225 RIAEAKLTSVPKGL---PPTLLELHLDYNKISTVELEDFKRYKELQRLGL-GNNKITDIE 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281 NGSLANIPRVREIHLENNKLKKIPSGL-PELKYLQIIFLHSNSIARVGVNDFCPTVPKMK 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323 D--LTGTANLESLTLTGAQISSLPQTVCNQLPNLQVLDLSYNLLEDLPSFSVCQKLQK-- 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 PPSCFSGLHSLRHLWLDDNALTEIPVQAFRSLSALQAMTLALNKIHHIPDYAFGNLSSLV 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 ELRIHENKVKKIQKDTFKGMNALHVLEMSANPLD------NNGIEPGAFEGVTVFHI 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 VLHLHNNRIHSLGKKCFDGLHSLETLDLNYNNLDEFPTAIRTLSNLKELG-----FH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 12.6%; Score 251.5; DB 2; Length 907; Best Local Similarity 24.6%; Pred. No. 2.4e-09; Matches 97; Conservative 59; Mismatches 122; Indels 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 CPFGCQCY--SRV---VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEND----
                                                                                                                                                                                                                                                                                                                          SFRDNQIKTINRNAFYDAASLVMLDLAKNQLTEIAPTTFLAQLNLLLVDL 371
                                                                                                                                                                                                                                                                                         ------KKSLYSAISLFNNPV---KYWEMQPATFRCVLSRMSVQL 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 -----FKGLTSLYGLILNNNKL--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phan G protein-coupled receptor precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    340 KSLYSAISLFNNPVKYWEMQPATFRCVLSRMSVQL 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----IDLRHNEI--YEIKVDTFQQLLSLRSLNL 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 HPKAFLTTKKLRRLYLSHNQLSEIPL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene: HG38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics:
                                                                                                                                                                                                                                                                                         339
                                                                                                                                                                                                                                                                                                                                               322
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A; Reference number: S42799
A; Reference number: S42799
A; Accession: S42799
A; Reference number: S42799
A; Accession: S47407
A; Accession: Accessio
               A Note: sequence extracted from NCBI backbone (NCBIP:110171)

C; Superfamily: leucine-rich alpha-2-glycoprotein repeat homology
F; 75-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F; 99-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F; 123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F; 171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F; 171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F; 195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F; 219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F; 242-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F; 267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F; 291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F; 315-388/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F; 333-362/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F; 363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F; 383-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F; 387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F; 387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Species: Homo sapiens (man)
C.Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jul-2000
C.Accession: S42799; I37407
                                                                                                                                                                                                                                                           <LRR5>
<LRR6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <LR16>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 PMCPFGCQCY-----SRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 SLGFLNLQGGQLGSLEPQALLGLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 SRLEDGLFEGLGSLWDLNLGWNSL---AVLPDAAFRGL-------GS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 LRELVLAGNRLAYLQPALFSGLAELRELDLSRNALRAIKANVFVQLPRLQKLYLDRNLIA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 KI-PSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQP 360
                                                                                                                                                                               homology <LRR3>
homology <LRR4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 SLYGLILLNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNL---PKSLAELRIHENKV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 KKIQKDTFKGMNALHVLEMSANPLDNNGIEP-GAFEGVTVFHIRIAEAKLTSVPKGLPPT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256 AVAPGAFLGLKALRWLDLSHNRVAGL-LEDTFPGLLGLR-----VLRLSHNAIA--SLRP 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <LR15>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 LLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 PACPAACVCSYDDDADELSVFCSSRNLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;411-434/Domain: leucine-rich alpha-2-91/coprotein repeat homology
F;435-458/Domain: leucine-rich alpha-2-91/coprotein repeat homology
F;435-482/Domain: leucine-rich alpha-2-91/coprotein repeat homology
F;485-506/Domain: leucine-rich alpha-2-91/coprotein repeat homology
F;507-529/Domain: leucine-rich alpha-2-91/coprotein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.3%; Score 246; DB 2; Length 605
25.3%; Pred. No. 3.4e-09;
tive 61; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Sratus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-662 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 ATFRCVLSRMSVQLGN 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 RTFKDLHFLEELQLGH 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80; Conservative
source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 SVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 AIPP-LPKKTTYFYSRFNRIKKINKNDFASLNDLKRIDLTSNLISEIDEDAFRKLPHLQE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 LYLSHNQLSEIPLNLPKSLAELRIHENKY--KKIQKDTFKGMNALHVLEMSANPLDNNGI 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 EPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGL 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------IPLPLPESLRALHLQNNDILEMHEDTFCNVKNLTYV-- 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.5%; Score 249; DB 2; Length 322;
27.9%; Pred. No. 9.2e-10;
ive 47; Mismatches 108; Indels 44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 DDDDDDDDDDDDDDDSDNSLFPTREPREFFFDL-----FPMCPFGCQCYSRVVHCSDLGLT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M86826; NID:9184807; PIDN:AAA36047.1; PID:9184808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteoglycan Lb precursor - mouse
N;Alternate names: chondroitin/dermatan sulfate proteoglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    272 GNNKITDIE-NGSLANIPRVREIHLENNKLKKIPSG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        288 -RKALEDIRLDGNPINLSRTPQAYM---CLPRLPIG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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O'Species: Mus musculus (house mouse)
C'Species: Was musculus (14130)
R'Ujita, M.; Shinomura, T.; Kimata, K.
Gene 158, 237-240, 1995
A'Title: Molecular cloning of the mouse osteoglycin-encoding gene.
A; Reference number: J04130
A; Molecular type: mRNA
A; Residues: 1-298 «UII»
A; Cross-references: DDBJ:D1951; NID:9971273; PIDN:BAA06721.1; PID:g1060928
C; Comment: This protein is a glycoprotein, belonging to the leucine-rich family. It is
C; Superfamily: osteoinductive factor precursor; leucine-rich alpha-2-glycoprotein rep
C; Reywords: chondroitin sulfate proteoglycan; glycoprotein
F; 1-19/Pomain: signal sequence #status predicted <AMI>F; 20-254/Region: leucine-rich
F; 144-167/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>F; 101/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
F; 258/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                          159 STLEDGLFEGLGNLWDLNLGWNSL---AVLPDAAFRGL--------GG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                 264
                                                                                                                               126 SLYGLILINNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLN---LPKSLAELRIHENKV 182
                                                                                                                                                                                                                                                              183 KKIQKDTFKGMNALHVLEMSANPLDNNGIEP-GAFEGVTVFHIRIAEAKLTSVPKGLPPT 241
                                                                                                                                                                                                                                                                                                                                                                                      LLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302 KI-PSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQP 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 SEIPLNLPKSLAELRIHENKVKK--IQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV 219
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                                        Gaps
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26.3%; Pred. No. 6.9e-09;
ive 44; Mismatches 128; Indels
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C;Species: Papio sp. (baboon)
C;Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
C;Accession: JG5239
R;Delhanty, P.: Baxter, R.C.
Biochem. Biophys. Res. Commun. 227, 897-902, 1996
A;Title: The cloning and expression of the baboon acid-labile subunit of the insulin-lik
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A; Residues: 1.605 <DEL>
C; Comment: This factor is structurally related to proinsulin and have insuline-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                  A; Cross-retrences: Subs. 4.3.911
A; Map position: 11q13.5-11q14
C; Superfamily: leucine-rich alpha-2-glycoprotein repeat homology CLRR1>
F; 50-73 Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR1>
F; 74-97 Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR2>
F; 14-97 Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR3>
F; 155-114 Pobmain: leucine-rich alpha-2-glycoprotein repeat homology CLRR4>
F; 155-113 Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR6>
F; 156-113 Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR6>
F; 165-124 Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR6>
F; 165-128 Domain: leucine-rich alpha-2-glycoprotein repeat homology CLRR6>
F; 265-289 Domain: leucine-rich alpha-2-glycoprotein repeat homology CLR10>
F; 316-339 Domain: leucine-rich alpha-2-glycoprotein repeat homology CLR10>
F; 316-336 Domain: leucine-rich alpha-2-glycoprotein repeat homology CLR12>
F; 367-386 Domain: leucine-rich alpha-2-glycoprotein repeat homology CLR15>
F; 340-36 Domain: leucine-rich alpha-2-glycoprotein repeat homology CLR15>
F; 341-433 Domain: leucine-rich alpha-2-glycoprotein repeat homology CLR15>
F; 441-46 Domain: leucine-rich alpha-2-glycoprotein repeat homology CLR15>
F; 45-49 Domain: leucine-rich alpha-2-glycoprotein repeat homology CLR15>
F; 45-49 Domain: leucine-rich alpha-2-glycoprotein repeat homology CLR15>
F; 45-514 Domain: leucine-rich alpha-2-glycoprotein repeat homology CLR15>
F; 55-75 Domain: leucine-rich alph
A;Cross-references: EMBL:Z24680; NID:g439295; PIDN:CAA80847.1; PID:g439296
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 SFLQPGAFQALTHLEHLSLAHNRLAMATALSAGGLGPLPRVTSLDLSGNSLYSGLLERLL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 CQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------EIPL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 NLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIR 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 IAEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYK-ELQRLGLGNNKITDIENGSL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 LSRNSLTCISDFSLQQLRVLDLSCNSIEAFQTASQPQAEFQLTWLDLRENKLLHFPD--L 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 PMCPFGCQC-YSRVVH-----CSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLT 125
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; Pred. No. 7.4e-09;
59; Mismatches 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.3%; Score 245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         285 ANIPRVREIHLENNKLKKIPSGLPE 309
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26.3%;
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                                                                                             A; Gene: GDB: GARP; D11S833E
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Db 265ERIEEIRLEGNPIALGKHPNSFICLKRLPI 294	eucine-rich alpha-2-glycoprotein repeat eucine-rich alpha-2-glycoprotein repeat eucine-rich alpha-2-glycoprotein repeat
RESULT 38 134555 hypothetical protein DKFZp434N0435.1 - human C;Species: Homo sapiens (man) C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T34555 R;Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.	alpha 2-giycoprotein repeat homology alpha-2-giycoprotein repeat homology
submitted to the Protein Sequence Database, October 1999 A;Reference number: 221540 A;Accession: T34555 A;Status: preliminary	Query Match Best Local Similarity 23.2%; Pred. No. 3.5e-08; Matches 85; Conservative 50; Mismatches 125; Indels 106; Gaps 8;
A;Molecule type: mRNA A;Residues: 1-333 <pous A;Cross-references: EMBL:AL122074 A;Experimental source: adult testis; clone DKF2p434N0435</pous 	Oy 75 PFGCQCYSRVVHCSDLGLTSVPTNIP
C; Generics: A; Note: DKFZp434N0435.1 Query Match 11.7%; Score 234; DB 2; Length 333;	QY 103 TRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFL 146
Similarity 24.0%; Pred. No. 1e-08; 9; Conservative 58; Mismatches 114; NNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTK	QY 147 TTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSA 203 DD 122 HLAALESLHLQCNQLQALPRRLEQPLTHLKTLNLAQNILLAQLPEELFHPLTSLQTLKLSN 181
Db 12 DISKNQISDIAPDAFQGLKSLTSLVLYGNKITEIAKGLFDGLVSLQLLLLNANKINCLRV 71 Qy 167 NLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNG 210	OY 204 NPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRY 263
:     : :       : :	264
132 IETSGARCSSPRRLANKRISQIKSKKFRCSGSEDYRSRFSSECFMDLVCPEKCRCEGTIV 1	308PELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLENNPVKYWEM
QY 226 -IAEAKLISVPKGLPPTLLELHLDYNKISTVELED-FRRYKELORLGLGNNKITDIENGS 283	Db 280 LETVTEGTFAHLSNLRSLMLSYNAITHLPAGIFRDLEELVKLYLGSNNLTAL 331 Qy 359 QPATFR 364
e e	332
340 KSLYSAISLENNPVKYWEMQPATFRCVLS 368	RESULT 40 113852 gene wheeler protein - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
17.3) 83K chain - human vision 20-Jul-1990 #text_change 05-Nov-1999	C. Accession: T18852 R.Eldon, E.; Kooyer, S.; D'evelyn, D.; Duman, M.; Lawinger, P.; Botas, J.; Bellen, H. Development 120, 885-899, 1994 A.Title: The Drosophila 18 wheeler is required for morphogenesis and has striking sim A; Reference number: Z17796; MUID: 95324375; PMID: 7600965 A; Accession: T18852 A; Status; preliminary; translated from GB/EMBL/DDBJ
R;Tan, F.; Weerasinghe, D.K.; Skidgel, R.A.; Tamel, H.; Kaul, R.K.; Roninson, I.B.; Schi J. Biol. Chem. 265, 13-19, 1990 A;Title: The deduced protein sequence of the human carboxypeptidase N high molecular wei A;Reference number: A34901; MUID:90094386; PMID:2378615 A;Accession: A34901 A;Status: preliminary	A;Molecule type: mRNA A;Residues: 1-1389 <eld> A;Cross-references: EMBL:L23171; NID:g415682; PID:g1019104; PIDN:AAA79208.1 C;Genetics: A;Gene: wheeler A;Cross-references: FlyBase:FBgn0004364</eld>
A;Molocule type: mkNA A;Residues: 1-556 <tany A;Cross-references: GB:J05158; NID:g179935; PIDN:AAA51921.1; PID:g179936 C;Genetics: Approximate the constant of the constant of</tany 	Query Match Best Local Similarity 25.9%; Pred. No. 2.5e-07; Matches 66; Conservative 43; Mismatches 95; Indels 51; Gaps 3;
A;Gene: GDB:ACBP A;Cross-references: GDB:127893 A;Cross-references: GDB:127893 C;Map position: 6q25.3-6q26 C;Superfamily: leucine-rich alpha-2-glycoprotein repeat homology C;Keywords: hydrolase; metallo-carboxypeptidase F;77-100/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lrri></lrri>	QY 106 LDLQNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIP 165

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A;Cross-references: EWBL:AF054827; NID:g3293317; PIDN:AAC25697.1; PID:g3293318
R;Sieburth, D.S.; Sun, Q.; Han, M.
Cell 94, 119-130, 1998
A;Title: SUR-8, a conserved Ras-binding protein with leucine-rich repeats, positively A;Reference number: Z22331; MUID:98337190; PMID:9674433
A;Accession: T43192
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AF068919; NID:93252976; PIDN:AAC39129.1; PID:93252977
C;Genetics:
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A;Experimental source: clone M88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein M88.6b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 15-Oct-1999
C;Accession: T23841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             345 IGIFSKATRLTKLNLKENELVSLPLDMGSWTSITELNLSTNQLKVLP-EDIEKLVNLEIL 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         404 VLSNNQLKKLPN-QIGNLNKLRELDLEENELETVPTEIGFLQHLTKLWYQSNKILTLPRS 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 RDSTVNVLPQDLFE-----NVFAKQVKLERCGLSTLQPNSFQSLGGSAELLSLRENRIK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 YSRVVHCSD-LGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKLTK 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 FIVESNHLQLLPPNLLTMLPKIHTVNLSRNELTAFPAGGPQQFVSTVTINMEHNQISKIP 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270 GLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSI----- 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 REPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTN----IPFDTRMLDLQNNKIK 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 -GAFEGVT-VFHIRIAEAKLTSVP--KGLPPTLLELHLDYNKISTVELEDFKRYKELQRL
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A;Map position: 3
A;Introns: 40/3; 60/2; 101/3; 216/2; 290/1; 361/1; 411/3; 455/1; 544/3
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                                                                                                                                                                                                                                                                                                                                                                                                Length 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                  67; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                             11.2%; Score 223; DB 2; 24.9%; Pred. No. 1.1e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: Z19806
A; Accession: T23841
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----ARVGVNDFCPTVPKMKKSLYSAISLFNN 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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A; Molecule type: mRNA
A; Residues: 1-559 <SEL>
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                                                                                                                                                                                                                                     A; Molecule type: mRNA
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R.Chiang, C.; Beachy, P.A.
R.Chiang, C.; Beachy, P.A.
A.Title: Expression of a novel Toll-like gene spans the parasegment boundary and contrib
A.Reference number: 217805; WUID:95151581; PMID:7848870
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C'Species: Caenorhabditis elegans
C'Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C'Accession: T42998; T43192
R'Selfors, L.M.; Schutzman, J.L.; Borland, C.Z.; Stern, M.J.
Proc. Natl. Acad. Sci. U.S.A. 95, 6903-6908, 1998
A;Title: Soc-2 encodes a leucine-rich repeat protein implicated in fibroblast growth A;Reference number: Z22280; MUID:98284030; PMID:9618511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tlr protein - fruit fly (Drosophila melanogaster)

'Species: Drosophila melanogaster

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000

C;Accession: T13887
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| | | : | | | : | 300 KGLLHRLEQLLYLDLSGNQLTSHYDNSTFAGLIRLIYLNYLNLSNNALTRIGSKTFKELYFL 359
                                                                       HVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKISTVE 256
                                                                                                                                                                              257 LEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSGLPELKYLQII 316
                                                                                                                                                                                                            | | :| | | | :| :| | :| | :| | :| | 398 NRIFNGLYVLTKLTLNNNLVSIVESQAFRNCSDLKELDLSSNQLTEVPEAVQDLSMLKTL 457
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                                                                                                         360 QILDMRNNSIGH--IEEGAFLPLYNLH---
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A;Cross-references: FlyBase:FBgn0004364
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Best Local Similarity
Matches 66; Conserv
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Οy	172 LAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKL 231	A; Exp	erj
Db	201 LKKLTLQNCNLEIIQKGAFRGLNSLEQLILSNNNLENIDWTIFSALKNLRV 251	A; Map po	] d
ΟŸ	232 TSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVR 291	A; Int A; Not	ror e:
QQ	252	Query	ry.
Qy	292 EIHLENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDF 331	Matche	che
Dp	296 VALFDRNKIESIGDMDMFGLTRSDRIETLSLARNNLSQISPKAF 339	Qy	œ
		ΩD	17
RESULT T23836	4	QY	14
C; Spe	ltis elegans	qa	23
C; Da C; Ac	s: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 sssion: T23836	Qy	18
R;Su Subm	R;Sulston, J. Submitted to the EMBL Data Library, June 1994	qq	29
A; Re	ssion: T23836	Qy	21
A; SC A; MO	A)Status: preliminary; translated from GB/EMBL/DDBU	qq	35
A; Re: A; Cr(	A; RESIGUES: 1-010 CMIL. X/Cross-references: EMBL: Z34802; PIDN: CAA84337.1; GSPDB: GN00021; CESP: M88.6a	Qy	27
C; Ge	Stimental Source: Cloue Moo	qq	40
A;Gel A;Maj A·⊺n	A; Gene: CESP: Md8.ba A; Map position: 3 A: Introns: 40/2: 60/2: 101/2: 216/2: 200/1: 427/2: 471/1: 560/2	QY	32
o you	tch 11.2%; Score 223; DB 2; Length 610; al Similarity 26.1%; Pred. No. 1.3e-07;	qq	46
Ma	; Conservative 59; Mismato	RESULT A88684	H 4
Oy Db	59 REPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLDUNNKIK 114   :	protein C;Specie C;Date:	in cie
ΟŊ	EIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKS	C; Acc R; and Scien	nym ce
QQ	141 KLEKGLFTGLKSLKTLDLAMNKIQEIDVGAFEELKKVEELLLNENDIRVLKTGTFDGMKN 200	A;Tit A:Ref	le
QY Dp	172 LAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKL 231   :  : ::      :    :    :    :    :	A; Note: A; Note: A; Access	e e e e
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δō i	TSVPKGLPPTLEELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVR	A; MO] A; Res	ecu
QD	252LDLGSNKISNVEMKSFPKLEKLVLNNNTIDSMKSIKLKDLPSLV 295	A;Cross- C;Geneti	etj
Qy G	292 EIHLENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDF 331	A;Gene: A;Map pc	o
RESULT	45	Query Best Match	Query Best I Matche
T309. hypot	7 - Caenorhabditis elegans	QY	œ
C; Spr C; Dad	C:Species: Caenornabolitis elegans C.Jotte: 22.Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999 C.Accasion: 731047	qu	22
R; Ne.	SOD, J.; Hawkins, J. Son, J.; Hawkins, J. Thed to the RMBL Data Library, June 1000	QY	14
A; Des	original The sequence of C. elegans cosmid AC7.	qa	27
A; Acc A; Sta	A;Accession: T30947 A;Status: preliminary; translated from GB/EMBL/DDBJ	Qy	18

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: Genome sequence of the nematode C. elegans: a platform for investigating blo ence number: A75000; MUID:99069613; PMID:9851916 see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; slon: A88684
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ies: 1-613 <STO>
references: GB:chr_IV; PIDN:AAB03418.1; PID:g1401355; GSPDB:GN00022; CESP:AC7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
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10-May-2001 #text_change 10-May-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----TFKGMNALHVLEMSANPL-------DNNGIEP-- 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 FIVESNHLQLLPPNLLTMLPKIHTVNLSRNELTAFPAGGPQQFVSTVTINMEHNQISKIP 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 -GAFEGVT-VFHIRIAEAKLTSVP--KGLPPTLLELHLDYNKISTVELEDFKRYKELQRL 269
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ns: 61/3; 105/3; 161/3; 234/1; 301/3; 375/1; 500/1
AC7.2
                                                                                                          references: EMBL:U61957; PIDN:AAB03417.2 mental source: strain Bristol N2; clone AC7
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282, 2012-2018, 1998
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le type: DNA
es: 1-572 <NEL>
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osition: 4
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F;79/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Matches 90; Conservative
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Best Local Similarity 24.19
Matches 84; Conservative
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                                                                                                                                                                                                Query Match
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A; Molecule type: protein
A; Experimental Source: Done
B; Experimental source: Done
R; Bentz, H.; Nathan, R.M.; Rosen, D.M.; Armstrong, R.M.; Thompson, A.Y.; Segarini, P.R.;
A; Blod. Chem. 264, 20805-20810, 1989
A; Title: Purification and characterization of a unique osteoinductive factor from bovine
A; Reference number: A32691; MUID:90062228; PMID:2584240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Bos primigenius taurus (cattle)
C; Date: 14-Sep-1990 #text_change 24-Sep-1999
C; Date: 14-Sep-1990 #sequence_revision 14-Sep-1990 #text_change 24-Sep-1999
C; Accession: A35272; A35561; A32691; B35379; B46743
R; Madisen, L; Neubauer, M; Plowman, G; Rosen, D.; Segarini, P.; Dasch, J.; Thompson, DNA Cell Biol. 9, 303-309, 1990
A; Title: Molecular cloning of a novel bone-forming compound: osteoinductive factor.
A; Reference number: A35272; MUID:90321465; PMID:2372374
   331 FIVESNHLQLLPPNLLTMLPKIHTVNLSRNELTAFPAGGPQQFVSTVTINMEHNQISKIP 390
                                                                                                                  270 GLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIARV--G 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M37974; NID:g163429; PIDN:AAA30670.1; PID:g163430 R;Bentz, H.; Chang, R.J.; Thompson, A.Y.; Glaser, C.B.; Rosen, D.M. J. Biol. Chem. 265, 5024-5029, 1990 A;Title: Amino acid sequence of bovine osteoinductive factor. A;Reference number: A35561; MUID:90202980; PMID:2180954
                                                                      214 -GAFEGVT-VFHIRIAEAKLTSVP--KGLPPTLLELHLDYNKISTVELEDFKRYKELQRL
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A; Residues: 1-299 <MAD>
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Cispedies: Mus musculus (house mouse)
Cispedies: Mus musculus (house mouse)
Cispedies: O7-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
Ciscession: A47530
Ribard, D.D.; Rongnoparut, P.; Allwardt, B.A.; Marton, L.S.; Stefansson, K. Genomics 17, 604-610, 1993
A;Title: The oligodendrocyte-myelin glycoprotein of mouse: primary structure and gene A;Reference number: A47530; MUID:94063902; PMID:8244377
                                                                                                                                                                                                                                                    13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
F:215/Binding site: carbohydrate (Asn) (covalent) #status absent
F:246,259/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:256-289/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTK 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 VDIDAVPP-LPKESAYLYARFNKIKKLTAKDFADIPNLRRLDFTGNLIEDIEDGTFSKLS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 NNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQ 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----SVPLNLPESLRVIHLOFNNITSITDDTFCKAND-- 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 TKEKETMIIVPDEKSFQLQKDENITPLPPKKEN-----DEMPTCLL-CVCLSGSVYCEE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 ILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQK-DT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 FKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDY 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 NKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIP-SGLP 308
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 AYQWN-LKYLDVSKNMLEKVVLIKNTLRSLEV--LNLSSNKLWTVPTNMPS---KLHI-- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBIP:140267)
                                                                                                                                                                                                                                                                                                                              ---FFSPSHIALKNMMLKDMEDTDDD--- 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 ICPLQCTCTERHRHVDCSGRNLTTLPPG-----LQENIH-----L 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:S67043; NID:9456806; PIDN:AAB28991.1; PID:9456807
A;Experimental source: C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 LLEELTLAENQLIKLPV-LPPKLTLFNAKYNKIKSRGIKANTFKKLHNLSFLY----LD
                                                                                                                                                                                                                                                                                                                                                                                                     LLLFLFVPLIKPAPPSQQDSRIIYDYGTDNLEETFFS-----QDYEDKYLDGKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDFPDLFPPDLFPMCPFGCQCYSRVVHCSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 KLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKK--IQKDTFKGMNALHVLEMSANPLD
                                                                                                                                                         ; Score 218; DB 2; Length 299;
; Pred. No. 1.1e-07;
44; Mismatches 114; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.9%; Score 216.5; DB 2; Length 440; 24.1%; Pred. No. 2.3e-07; Live 46; Mismatches 115; Indels 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIGIGNNKITDIENGSLANIPRVREIHLENNK--LKKIPSGLPELKYLQI 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----TSYIRD-----RIEEIRLEGNPVILGKHPNSFICLKRLPI 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Note: sequence inconsistent with nucleotide translation A; Note: sequence extracted from NCBI backbone (NCBIN:139694, NCB C; Superfamily: leucine-rich alpha-2-glycoprotein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oligodendrocyte-myelin glycoprotein, mOMgp - mouse
                                                                                                                                                             10.9%; 25.7%;
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A; Molecule type: mRNA
A; Residues: 1-1535 <NEL>
A; Cross-references: GB:U11052; NID:9531384; PIDN:AAA61568.1; PID:9531385
C; Superfamily: peroxidasin; myeloperoxidase homology; proteoglycan amino-terminal homolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: AD1822
K;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.: Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, G
DNA Res. 8, 205-213, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Nelson, R.E.; Fessler, L.I.; Takagi, Y.; Blumberg, B.; Keene, D.R.; Olson, P.F.; Parke
EMBO J. 13, 3438-3447, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Nostoc sp. A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: GB:BA000019; PIDN:BAB77648.1; PID:g17135102; GSPDB:GN00179 A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Peroxidasin: a novel enzyme-matrix protein of Drosophila development. A;Reference number: S46224; MUID:94341255; PMID:8062820 A;Accession: S46224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peroxidasin - fruit fly (Drosophila sp.)
C;Species: Drosophila sp.
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Oct-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 AKLTNLTRENLSYNQRTEIPEALAKLTNLTQLILSDNQIKEIPETIAKLTNLTHLI-LSG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326 P-EAITKLTHLILSGNQIKEIPE-TIAKLTNLTQLALSSNQITEIPEVLAQLTNLTQ 383
--VDLSNNSLTQILPGTLINLTHLTHLYLHNNKFTFIPEQSFD 212
                                                              ----SIARVGVNDFCPTVPK 337
                                                                                                                   213 OLLOLOEITLHNNRWSCDHKONITYLLKWVMETKAHVIGTPCSKOVSSLKEOSMYPTPPG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 LTSVP-----TNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 ITEIPEALAKLTNL----TQLNLSYNQITEIPEALAK-LTNLTQLNLRGNQRTEI-PEAL 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 LTTKKLRRLYLSHNQLSEIPLNLPK--SLAELRIHENKVKKIQKDTFKGMNALHVLEMSA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 NPLDN-----NGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKISTV 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256 ELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSGLPELKYLQI 315
                                                                                                                                                                                                                                                                                                                                                                                                          leucine-rich-repeat protein [imported] - Nostoc sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 1119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.9%; Score 216.5; DB 2; Length 1 30.7%; Pred. No. 7.7e-07; ive 47; Mismatches 94; Indels
                                                                                                                                                                                                                         273 FTSSLFTMSEMQTVDTINSLSMVTQPKVTKTPKQYRGKETTFGVTLSK 320
                                                                                                                                                                                    338 MKKSLY-----SAISLFNNP----VKYWEMQPATFRCVLSR 369
                                                           309 ELKYLQIIFLHSN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316 IFLHSNSIARV 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384 LFLSSNQITQI 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-1119 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 77; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: alr0124
172 ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 50
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4;
                                                                                                                                              74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                        26 CPAGCTCLERTVRCIRAKLSAVP-KLPQDTQTLDLRFNHIEELPANAFSGLAQLTTLFLN 84
                                                                                                      33;
                                                             Length 1535;
                                                                                                                                                                                                                                                                                                                                        145 DNLPR-LNRLIMYNNKLTQLPVDGFNRLNNLKRLRLDGNAIDIDCNCGV 192
                                                                                                                                                                                                                                                                                                                  167 -NLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLD---NNGI 211
                                                                                                      Indels
F;19-44/Domain: proteoglycan amino-terminal homology <PAH4> F;661-1350/Domain: myeloperoxidase homology <MPX>
                                                               DB 2;
                                                                                     Pred. No. 1.4e-06;
                                                                                                                                                                                                                               134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPL------
                                                             10.8%; Score 215.5; D
32.5%; Pred. No. 1.4e-
ive 25; Mismatches
                                                                                 Local Similarity 32.5%
hes 55; Conservative
                                                             Query Match
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Search completed: January 24, 2003, 12:27:32 Job time: 29 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

January 24, 2003, 12:21:30 ; Search time 14 Seconds (without alignments) 1122.823 Million cell updates/sec Run on:

US-09-944-457-2 1992 1 MKEYVLLFFLALCSAKPFFS......PATFRCVLSRMSVQLGNFGM 379 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Q9bxn1 homo sapien	_	Q9ib75 xenopus lae	P47853 rattus norv	P28653 mus musculu	P21810 homo sapien	_	046390 ovis aries	002678 canis famil	P21809 bos taurus	Q9de68 coturnix co	P28675 gallus gall		P07585 homo sapien	ovis	P21793 bos taurus	Q28888 oryctolagus		Q29393 canis famil	P28654 mus musculu	Q01129 rattus norv	Q9gkq6 sus scrofa			Q9de67 coturnix co	P51884 homo sapien		snw	P51886 rattus norv	Q99983 homo sapien	l homo	n8 bos t	P51888 homo sapien
ΔΙ	ASPN_HUMAN	ASPN_MOUSE	PGS1_XENLA	PGS1_RAT	PGS1_MOUSE	PGS1_HUMAN	PGS1_HORSE	PGS1_SHEEP	PGS1_CANFA	PGS1_BOVIN	PGS2_COTJA	PGS2_CHICK	PGS2_PIG	PGS2_HUMAN	PGS2_SHEEP	PGS2_BOVIN	PGS2_RABIT	PGS2_HORSE	PGS2_CANFA	PGS2_MOUSE	PGS2_RAT	PGS1_PIG	PGS1_RABIT	LUM_CHICK	LUM_COTJA	LUM_HUMAN	LUM_BOVIN	LUM_MOUSE	LUM_RAT	OMD_HUMAN	FLR1_HUMAN	PRLP_BOVIN	PRLP_HUMAN
DB	Н	Н	Н	Н	Н	-1	Н	Н	Н	Н	<del>,  </del>	Н	,	<del>,  </del>	Н	-	Н		-	Н	<del>, ,</del>	Н	-	-	-	Н	-	H	Н	-	Н	Н	-
Length	379	373	368	369	369	368	372	369	369	369	356	357	360	359	360	360	360	360	360	354	354	272	135	343	343	338	342	338	338	421	646	381	382
& Query Match	0	90.3	7	2	ä	ä	i,	ä	٠	Ϊ.	48.9		48.5	48.4	•	•	47.2	7.		ς.	2	ς.	ς.		。	σ	ó.	6	6	•	18.2		18.0
Score	1992	1799	7	1040.5	1037.5	1034	1028.5	1027.5	_	1019.5	974	696	an.	963.5	947	943	941	939		907.5	899	641	4	399.5	8	390	384	383	378	366	363.5	361.5	358.5
Result No.	1	7	က	4	ស	9	7	89	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

Q9eqp5 rattus norv	035367 mus musculu	P13605 bos taurus	_	_	_		077742 bos taurus	-		P50608 mus musculu	042235 gallus gall	Q9de66 coturnix co	Q06828 homo sapien	P24014 drosophila	043155 homo sapien	035103 mus musculu
PRLP_RAT .	KERA_MOUSE	FMOD_BOVIN	PRLP_MOUSE	KERA_BOVIN	KERA_HUMAN	FMOD_RAT	OMD_BOVIN	FMOD_CHICK	FLR3_HUMAN	FMOD_MOUSE	KERA_CHICK	KERA_COTJA	FMOD_HUMAN	SLIT_DROME	FLR2_HUMAN	OMD_MOUSE
	Н	<del>,</del> 1	Н	_	Н	щ	~	Н		-	-	Н	-	-	~	П
17	351	375	378	352	352	376	422	380	649	376	353	353	376	1480	099	423
'n																
	17.3	17.2	17.2	17.1	17.1	17.0	17.0	16.7	16.6	16.6	16.3	16.3	16.3	15.9	15.7	15.4
17.9	17.3	342.5 17.2					338 17.0		331.5 16.6		325 16.3				313.5 15.7	

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                        -!- PTM: Does not contain a serine/glycine dipeptide sequence required for the assembly of 0-linked glycosaminoglycans and is probably not a proteoglycan. The N-linked glycan at Asp-281 is composed of variable structures of GlcNAc, mannose, fucose, HexNAc and hexose -!- POLYMORPHISM: The poly-Asp region of ASPN is polymorphic and ranges at least from 11 to 17 Asp.
-!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
                                -i- TISSUE SPECIFICITY: Higher levels in osteoarthritic articular cartilage, aorta, uterus. Moderate expression in small intestine, heart, liver, bladder, ovary, stomach, and in the adrenal, thyroid, and mammary glands. Low expression in trachea, bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEND 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
discovered member of the leucine-rich repeat protein family."; J. Biol. Chem. 276:12212-12221(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein; Extracellular matrix; Signal; Repeat;
Leucine-rich repeat; Polymorphism; Triplet repeat expansion.
SIGNAL 1 14 POTENTIAL.
PROPEP 15 32 POTENTIAL.
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                                                                                                                                                                       (SLRPS) FAMILY. CLASS I SUBFAMILY.
-!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O-LINKED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 786625859E26A96D CRC64;
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InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Nterm.
                                                                                                                                                                                                                                                                                                 EMBL; AF316824; AAK35161.1; -. EMBL; AY029191; AAK31800.1; -. EMBL; AK027359; BAB55060.1; -.
                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
Pfam; PF00560; LRR; 8.
Pfam; PF01462; LRRNT; 1.
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SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_TYP; 7.
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A Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
A Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Arakawa T., Hara A., Fukunishi Y., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,
A Kuchl P., Lewis S., Matsuo Y., Gissi C., King B., Kochiwa H.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Blake J., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
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61 PRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEND 120
                                                                                                                  FKGLTSLYGLILUNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHEN 180
                                                                                                                                                                                                121 FKGLTSLYGLILUNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHEN 180
                                                                                                                                                                                                                                                                              240
                                                                                                                                                                                                                                                                                                                                                                                                                                          241 TLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentía; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                              181 KVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPP
                                                                                                                                                                                                                                                                                                                           181 KVKKIOKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 TLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQP
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MEDLINE=21192276; PubMed=11152692;
Lorenzo P., Aspberg A., Oennerfjord P., Bayliss M.T., Neame P.J.,
Heinegaard D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                099M04; 09D6A2;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE.
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MEDLINE=21085660; PubMed=11217851;
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Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Borls A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y., "Functional annotation of a full-length mouse cDNA collection.";
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- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
- (SLRPS) FAMILY. CLASS I SUBFAMILY.
  SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
  CAUTION: Ref.3 sequence differs from that shown due to a stop codon in position 238.

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Glycoprotein; Extracellular matrix; Signal; Repeat; POTENTIAL. ASPORIN. CYS-RICH. LRR-S 1.
LRR-T 1.
LRR-T 2.
LRR-S 2.
LRR-T 3.
LRR-T 4. EMBL; AF316825; AAK35162.1; -. EMBL; AK014504; BAB29402.1; ALT\_TERM. MGD; MGI:1913945; Aspn.
InterPro; IPR001611; LRR.
InterPro; IPR00372; LRR.Nterm.
InterPro; IPR003592; LRR\_out.
InterPro; IPR003591; LRR\_typ.
Pfam; PF00560; LRR; B.
Pfam; PP01462; LRRNT; 1. SMART; SM00370; LRR; 3. SMART; SM00013; LRRNT; 1. SMART; SM00369; LRR\_TYP; 15 32 37 37 89 89 109 1157 1157 1157 127 202 Leucine-rich repeat. 16 33 76 89 1110 1134 1158 DOMAIN REPEAT PROPEP CHAIN 

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	Gaps	60 54	120	180	240	300	360	
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); (POTENTIAL)	373;	NSLF 	CIKEL	AELR       AELR	SVPK	THLE 	VKYW :    MKYW	
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SIMILARITY) NAG) (	Len	gac	RMLD   :   RMVD	SIPLN 	IIRIA       IRIA	LANI	SAIS	
IMIL? RAC	B 1; -117; 14;	DDDDD  - - - DDDDNI	IPFD1	NOLSE NOLSE NOLSE	VTVE       VTVE	IENGS   - -: IENGI	KKSLY       KKSLY	
RITY. (BY S (GLCN	); D 2.5e	EDTO IIII	NTGN:	YLSH       YLSH	AFEG       AFEG	KITD :    RITD	VPKM 	
-S 3. -T 5. -T 6. -S 4. -T 7. -T 8. -T 8. SIMILARITY SIMIL	1799 No. smatc	MLKDN           MLKDN	LGLTS	KLRRI       KLRRI	GIEPO	GLGN	DFCP1       DFCP1	
LRR-T 5.  LRR-T 6.  LRR-T 6.  LRR-T 7.  LRR-T 7.  LRR-T 8.  POLY-ASP.  POLY-ASP.  O-LINKED (BY SIMILARITY).  O-LINKED (GACONAC ) (PACONAC.	Score 1799; DB 1; Pred. No. 2.5e-117; 17; Mismatches 14;	ALKNM 	/HCSD	TLTTK	DLDNN   :     crn	SLORL        SLORL	RVGVN      KVGVN	
MW;	88; 88; 17;	PSHIA	YSRV         YSRV	HPKAH	MSANI         	KRYKI    :  KRYRI	NSIAH         SIAH	378
148 172 196 119 49 73 446 759 42572	90.3%; 90.2%; ive	(PFFS       (PFFS	2025 1111 2025 2025	CLTKI        LTKI	CHVLE	SLEDF       SLEDL	FLHS	
	ty erval	LCSAI :       VCSAI	PMCPI      PTCPI	LNNN	GMNAI      GMNAI	ISTVI       ISTVI	YLOII YLOII	VOLGP VOLGP VOLGP
228 249 273 297 320 350 356 326 48 275	Llari Cons	LEELA 	PFDLF  - - -	YGLI	CDTFK	DYNK   :    DFNK	PELK       QELK	SRMS
	ch 1 Similarity 90 341; Conservative	MKEYVLLEFLALCSARPEFSPSHIALKNWMLKDMEDTDDDDDDDDDDDDDDDDDSDNSLFPTRE      :     :     :	PRSHFFFFDLFPMCPFGCQCYSRVYHCSDLGLTSVPTNIPFDTRMLDLQUNKIKEIKEND   :	FKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSBIPLNLPKSLAELRIHEN 	KVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPP 	TLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKL 	KKIPSGLPELKYLOIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYMEMQP 	ATFRCVLSRMSVQLGNFG                ATFRCVLGRMSVQLGNVG
REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT DOMAIN DISULFID CARBOHYD CARBOHYD SEQUENCE	at ()	1 MK	61 PR       55 PV	121 FK 	181 KV     15 KV	241 TL 	301 KK    295 KK	361 AT    355 AT
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FT FT FT FT FT SO	OME	Qy Dp	Qy Db	Qy Db	Qy Dp	Qy Db	Qy	Qy Db

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15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 368 AA. Xenopus laevis (African clawed frog). PRT; STANDARD; Biglycan precursor. PGS1\_XENLA Q9IB75; RESULT 3 PGS1\_XENLA

Eukaryota; Metažoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mombibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus. NCBI\_TaxID-8355; SEQUENCE FROM N.A. GOOD T. Kubota H.Y.; "CDNA of biglycan of Kenopus laevis."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.-!- FUNCTION: May be involved in collagen fiber assembly (By similarity) 

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation --:- SUBCELLULĀR LOCATION: Extracellular matrix (By similarity).
-:- SIMILARIY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
(SLERE) FAMILY. CLASS I SUBFAMILY.
-:- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).

REPEAT REPEAT

REPEAT REPEAT REPEAT

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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 IAEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLA 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 DDEDNSL--FPTRE-PRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRM 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 LDLQNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 VSEAKLSGIPKGLPSTLNELHLDNNKIQAIEKEDLSQYASLYRLGLGHNNIRMIENGSLS 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286 NIPRVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                   Interpro; IPR00151; LRR.
Interpro; IPR00152; LRR.Nterm.
R Interpro; IPR000372; LRR.Nterm.
Interpro; IPR003591; LRR.Nterm.
Interpro; IPR003591; LRR.ytp.
R Pfam; PF001560; LRRR; 9.
R Pfam; PF001560; LRRR; 1.
SMART; SM0001370; LRRR; 1.
SMART; SM0001370; LRRR; 1.
R SMART; SM0001370; LRRNY; 1.
R SMART; SM0001370; LRRNY; 1.
R SMART; SM0001370; LRRNY; 1.
R SMART; SM001369; LRRNY; 1.
R SMART; SM001369; LRRNY; 1.
R SIGNAL 1 19 POTENTIAL.
I 19 PROPEP 20 7 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.4%; Score 1044; DB 1; Length 3
58.1%; Pred. No. 3.3e-65;
ive 61; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53ADF7E7E3BDC528 CRC64;
                                                                                                                                                                                                                                                                                                                                                                      LRR-S 3.
LRR-T 5.
LRR-T 6.
LRR-S 4.
LRR-T 7.
LRR-T 7.
BY SIMILARITY.
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BIGLYCAN.
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LRR-T
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                                                                               EMBL; AB037269; BAA90246.1; -.
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343
63
321
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127
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                                                                                                                                                                                                                                                                          -i- TISSUE SPECIFICITY: Found in several monecity tissues, specially in articular cartilages.
-i- PTM: The two attached glycosaminoglycan chains can be either chondroitin sulfate of dermatan sulfate (By similarity).
-i- SIMILARIY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SLRPS) FAMILY. CLASS I SUBFAMILY.
-i- SIMILARIY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                 Dreher K.L., Asundi V.K., Matzura D., Cowan K.;
"Vascular smooth muscle biglycan represents a highly conserved proteoglycan within the arterial wall.";
Eur. J. Cell Biol. 53:296-304(1990).
-!-FUNCTION: May be involved in collagen fiber assembly (By similarity).
-!-SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By
                                                                                                                                                                                                                                                    similarity).
-!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRR-T 8.
O-LINKED (GLYCOSAMINOGLYCAN) (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U17834; AAA56797.1; -.

R InterPro; IPR001611; LRR.

R InterPro; IPR00352; LRR.Nterm.

R InterPro; IPR003591; LRR.Ltp.

R InterPro; IPR003591; LRR.Ltp.

R InterPro; IPR003591; LRR.Ltp.

R Ffam; PF01462; LRR; 8.

R SMART; SM00013; LRR; 3.

R SMART; SM00013; LRR, 3.

R SMART; SM00369; LRR.Trp; 1.

R GMACOPTOTEN; EXTREDILULAR matrix; Proteoglycan; Repeat;

M Leucine-rich repeat; Signal.

P SIGNAL.

1 19 POTENTIAL.
             Biglycan precursor (Bone/cartilage proteoglycan I) (PG-S1).
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15-JUN-2002 (Rel. 41, Last annotation update)
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LRR-T 1.
LRR-T 2.
LRR-S 2.
LRR-T 3.
LRR-T 4.
LRR-T 4.
LRR-T 5.
LRR-T 6.
LRR-T 6.
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                                                                                                                      TISSUE-Vascular smooth muscle;
MEDLINE=91184222; PubMed=2081545;
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64
322
369 AA;
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                                                                               NCBI_TaxID=10116;
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                                                                                                                                                                                               230 ETLNELHLDHNKIQAIELEDLLRYSKLYRLGLGHNQIRMIENGSLSFLPTLRELHLDNNK 289
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                                                                                                                                                                                                                                         NKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLP 239
                                                                                                                                                                                                                                                                                                  240 PTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNK 299
                                                                                                                                                                                                                                                                                                                                                              LKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQ 359
                                                                             Saeaemaenen A.-M.K., Salminen H.J., Rantakokko A.J., Heinegaard D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Murine fibromodulin; cDNA and genomic structure, and age-related expression and distribution in the knee joint.";
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52.2%; Score 1040.5; DB 1; Length 369; 52.6%; Pred. No. 5.7e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biglycan precursor (Bone/cartilage proteoglycan I) (PG-S1).
                               93; Indels
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Submitted (JUL-1990) to the EMBL/GenBank/DDBJ databases.
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PGS1_MOUSE SIAM...
PG865; Q61855;
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last sequence update)
...w.-2002 (Rel. 41, Last annotation update)
...mr (Bone/cartilage proteoglyce
                              67; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-NIH Swiss; TISSUE-Fibroblast;
Naitoh Y., Suzuki S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=NIH Swiss; TISSUE=Embryo;
MEDLINE=94319093; PubMed=8043960;
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TISSUE=Breast, and Kidney;
                          Matches 199; Conservative
              Similarity
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                                                                                   -i- TISSUE SPECIFICITY: Found in several connective tissues, specially in articular cartilages.
-i- PTM: The two attached glycosaminoglycan chains can be either chondroitin sulfate or dermatan sulfate (By similarity).
-i- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SLRPS) FAMILY. CLASS I SUBFAMILY.
-i- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
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                                                                  SUBCELLULAR LOCATION: Extracellular matrix (By similarity)
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Biochem. J. 355:577-585(2001).
-!- FUNCTION: May be involved in collagen fiber assembly (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01462; LRRNT; 1.
SMART; SM00370; LRR; 3.
SMART; SM00369; LRR_TYP; 1.
SMART; SM00369; LRR_TYP; 1.
G1ycoprotein; Extracellular matrix; Proteoglycan; Repeat; SIGNAL
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93; Indels
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4B57FCC9A1026BE6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Y11758; CAA72422.1; -. PIR; S20811; S30811. MGD; MGI:88158; Bgn. InterPro; IPR001611; LRR. InterPro; IPR000372; LRR_Nterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L20276; AAA64360.1; -. BC005452; AAH05452.1; -. BC019502; AAH19502.1; -.
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InterPro; IPR003591; LRR_typ.
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Mallon A.M., Platzer M., Bates R., Gloeckner G., Botcherby M., Nordalek G., Strivens M.A., Kloschis P., Dangel A., Cunningham D., Straw R., Weston P., Hunter C., Gilbert M., Fernando S., Goodall K., Kerry G., Greystrong J.S., Clark D., Goerdes M., Blechschmidt K., Rump A., Hinzmann B., Mundy C.R., Miller W., Poustka A., Herman G.E., Rhodes M., Denny P., Rosenthal A., Brown S.D.M.;
"Comparative genome sequence analysis of the Bpa/Str region in mouse
                                                                                                                                                                                                                                                                                                                  EPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEN 119
                                    60 -----FSAMCPFGCHCHLRVVQCSDLGLKTVPKEISPDTTLLDLQNNDISELRKD 109
                                                                       120 DFKGLTSLYGLILUNNKLTKIHPKAFLTTKKERRLYLSHNQLSEIPLNLPKSLAELRIHE 179
                                                                                             240 PTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNK 299
                                                                                                                                                                                                                                              300 LKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQ 359
                                                                                                                                                 180 NKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLP 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-91317791; PubMed-1860845;
Fisher L.W., Heegaard A.M., Vetter U., Vogel W., Just W.,
Termine J.D., Young M.F.;
"Human biglycan gene. Putative promoter, intron-exon junctions, and
chromosomal localization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fisher L.W., Termine J.D., Young W.F.; "Deduced protein sequence of bone small proteoglycan I (biglycan) shows homology with proteoglycan II (decorin) and several nonconnective tissue proteins in a variety of species."; J Biol. Chem. 264:4571-4576(1989).
                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Cranjata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGS1_HUMAN STANDARD; PRT; 368 AA.
P21810; P13247;
P01-JAN-1990 (Rel. 13, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Biglycan precursor (Bone/Cartilage proteoglycan I) (PG-S1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 266:14371-14377(1991).
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MEDLINE=20314869; Pubmed=10854409;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                               -!- TISSUE SPECIFICITY: Found in several connective tissues, specially
                                                                                                                            Fisher W.Y. Hawkins G.R., Tuross N., Termine J.D.;
"Purification and partial characterization of small proteoglycans I and II, bone staloproteins I and II, and osteonectin from the mineral compartment of developing human bine.";
J. Biol. Chem. 262:9702-9708(1987).
         MEDLINE=90073579; PubMed=2590169; Roughley P.J., White R.J.; "Dermatan sulphate proteoglycans of human articular cartilage. The properties of dermatan sulphate proteoglycans I and II.";
                                                                                                                                                                                                                                                                                                                                                                                                             -! - SUBCELLULAR LOCATION: Extracellular matrix (By similarity)
                                                                                                                                                                                                                                                              Just W., Rau W., Muller R., Geerkens C., Vogel W.; "Dinucleotide repeat polymorphism at the human biglycan (BGN)
                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: May be involved in collagen fiber assembly (By
                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By
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                                                                                                                                                                                                                                                                                                           Hum. Mol. Genet. 3:2268-2268(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, M65153; AAA52287.1; ALT_SEQ.
EMBL, M65152; AAA52287.1; JOINED.
EMBL, U82695; AAF33330.1; -
EMBL, BCO02416; AAH02416.1; -
EMBL; U11686; AAH0244.1; -
EMBL; U11686; AAC50117.1; -
                                                                                                                                                                                                                                                   MEDLINE=95187185; PubMed=7881444;
                                                                                                                 MEDLINE=87250639; PubMed=3597437;
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InterPro; IPR001611; LRR.
InterPro; IPR00372; LRR_Nterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
                                                                       Biochem. J. 262:823-827(1989).
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19 37
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368
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                                                                                                                                                                                                                     SEQUENCE OF 361-368 FROM N.A.
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PIR; A32458; A32458.
PIR; A40757; A40757.
PIR; S05639; S05639.
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"Dose dependent effects of corticosteroids on the expression of matrix related genes in equine articular chondrocytes.";
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                            ------AMCPFGCHCHLRVVQCSDLGLKSVPKEISPDTTLLDLQNNDISELRKDDF 110
                                                                                                                                                                                                                                                                                                                                                                                                          62 RSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDF 121
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                                                                                                                                                                                                                                                                                                                                                                                            122 KGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLK 301
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                                                                                                                                                                                                                                                                       93; Indels 20; Gaps
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Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                  O-LINKED (GLYCOSAMINOGLYCAN).
O-LINKED (GLYCOSAMINOGLYCAN).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Biglycan precursor (Bone/Cartilage proteoglycan I) (PG-SI).
                                                                                                                                                                                                                     BF16F304C5CD3B3E CRC64;
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-> DV (IN REF. 1).
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LRR-S 3.
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                                                                                                                                                                                                                    368 AA;
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O46403; Q9N1U5;
30-MAY-2000 (Rel
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SEQUENCE OF 150-192 FROM N.A. MEDLINE-20082971; Pubmed=10613847; Cactano A.R., Shlue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F., Bowling A.T., Murray J.D.; "A comparative gene map of the horse (Equus caballus)."; Genome Res. 9:1239-1249(1999).
                                                                                                                                                                                                                                                                                                                                                 -i- PTM: The two attached glycosaminoglycan chains can be either chondroitin sulfate or dermatan sulfate (By similarity).
-i- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                          similarity).
SUBCELLULAR LOCATION: Extracellular matrix (By similarity)
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                                                                                                                                                                                                 -!- FUNCTION: May be involved in collagen fiber assembly (By
                                                                                                                                                                                                                                                               SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        matrix; Proteoglycan; Repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SLRPS) FAMILY. CLASS I SUBFAMILY.
SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
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EMBL, AF135020, AAF64248.1; -.
INTECPTO: IPR001611, LRR.
INTECPTO: IPR00372; LRR.Neterm.
INTECPTO: IPR003592; LRR.LOUT.
INTECPTO: IPR003592; LRR.LOUT.
INTECPTO: IPR003591; LRR.LYP.
INTECPTO: IPR003591; LRR.LYP.
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 DFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHE 179
                                                          180 NKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLISVPKGLP 239
                                                                                                                                                          240 PTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNK 299
                                                                                                                                                                                                                LKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQ 359
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity)
-!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bruett L., Clements J.E.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May be involved in collagen fiber assembly (By
                                                                                                                                                                                                                                                                                                                                                                                                    30-WAY-2000 (Rel. 39, Created)
WAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Biglycan precursor (Bone/Cartliage proteoglycan I) (PG-S1).
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InterPro; IPR001611; LRR.
InterPro; IPR001372; LRR.Nterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
Pfam; PF01462; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                          51.6%; Score 1027.5; DB 1; Length 369;
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Biglycan precursor (Bone/cartilage proteoglycan I) (PG-S1).
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Pred. No. 4.5e-64;
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Matches 196; Conservative
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DFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHE 179
    54 DALTPTYS----AMCPFGCHCHLRVVQCSDLGLKAVPKEISPDTMLLDLQNNDISELRAD 109
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J. Biol. Chem. 264:2876-2884(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-96113563; PubMed-8673009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Cartilage;
MEDLINE=89255324; PubMed=2656687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Cartilage;
MEDLINE-89123388; PubMed=2914936;
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                                                                                                                                                                                                              360 PATFRCVLSRMSVQLGNF 377
                                                                                                                                                                                                                                    350 PATFRCVIDRLAIQFGNY 367
                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
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                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9913;
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                                                                                                . .) (POTENTIAL) . .) (POTENTIAL)
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                                                                    -!- FUNCTION: May be involved in collagen fiber assembly (By
                                                                                          SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; Extracellular matrix; Proteoglycan; Repeat; Leucine-rich repeat; Signal.
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                                                         Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases
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8C919E922D6377E6 CRC64;
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BY SIMILARITY.
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BY SIMILARITY.
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SIMILARITY)
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InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
Pfam; PF00560; LRR; 7.
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SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_TYP; 1.
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                                  SEQUENCE FROM N.A.
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Neame P.J., Choi H.U., Rosenberg L.C.;
"The primary structure of the core protein of the small, leucine-rich
proteoglycan (PG 1) from bothe articular cartilage.";
J. Biol. Chem. 264:8653-8661(1989).
230 ETLNEIHLEHDHNKIQAIELEDILRYSKLYRLGLGHNQIRMIENGSLSFLPTLRELHLDNNK 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yu J.H., Radhakrishnamurthy B., Srinivasan S.R., Berenson G.S.;
Primary structure of bovine aorta biglycan core protein deduced from
                                                        180 NKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFECVTVFHIRIAEAKLTSVPKGLP 239
                                                                                                                                240 PTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNK 299
                                                                                                                                                                                                        300 LKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQ 359
                                                                                                                                                                                                                             PGS1_BOVIN STANDARD; PRT; 369 AA. P21809; P79259; 01-MAY-1991 (Rel. 18, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation recursor (Bone/cartilage proteoglycan I) (PG-S1) (Leucinerich PG I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Characterization of the dermatan sulfate proteoglycans, DS-PGI and DS-PGII, from bovine articular cartilage and skin isolated by octyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reinboth B., Hanssen E., Cleary E.G., Gibson M.A.;
"Molecular interactions of biglycan and decorin with elastic fiber components: biglycan forms a ternary complex with tropoelastin and microfibril-associated glycoprotein 1.";
J. Biol. Chem. 277:3950-3957(2002).
-!- FUNCTION: May be involved in collagen fiber assembly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Choi H.U., Johnson T.L., Pal S., Tang L.H., Rosenberg L.C.,
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SEQUENCE FROM N.A.
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SUBUNIT: Forms a ternary complex with MFAP2 and ELN.
SUBCELLULAR LOCATION: Extracellular matrix.
TISSUE SPECIFICITY: Found in several connective tissues, specially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDF 121
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SWART; SW00013; LRRNT; 1.
SWART; SW00013; LRR_TYP; 1.
Glycoprotein; Extracellular matrix; Proteoglycan; Signal; Repeat;
Leucine-rich repeat.
SIGNAL
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-!- PTM: The two attached glycosaminoglycan chains can be either chondroith sulfate or dermatan sulfate.
-!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SLRPS) FAMILY. CLASS I SUBFAMILY.
-!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
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C -> E (IN REF. 2).
A -> R (IN REF. 2).
KK -> Y (IN REF. 2).
KK -> Y (IN REF. 2).
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InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_Out.
InterPro; IPR003591; LRR_typ.
Pfam; PF00560; LRR, T, P.
Pfam; PF01462; LRRNT; 1.
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369 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBCELLUIÂR LOCATION: Extracellular matrix (By similarity).
-1- PTM: The attached glycosaminoglycan chain can be either
chondroitin sulfate or dermatan sulfate depending upon the tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 RVPAGLPDLKLLQVVYLHTNNITKVGVNDFCPVGFGVKRAYYNGISLFNNPVPYWEVQPA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coturnix coturnix japonica (Japanese quail).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                KIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPA 361
                                                                                    182 VKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPT 241
                                                                                                                                                               172 IRKVPKGVFSGLRNMNCIEMGGNPLENSGFEPGAFDGLKLNYLRISEAKLTGIPKDLPET 231
112 KGLQHLYALVLVNNKISKIHEKAFSPLRKLQKLYISKNHLCEIPPNLPSSLVELRIHDNR 171
                                                                                                                                                                                                                                                    LLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUB-Cornea, and Sclera;
MEDLINE-20556471; PubMed-11102759;
Corpuz L.M., Dunleyy J.R., Hassell J.R., Conrad A.H., Conrad G.W.
"Molecular cloning and relative tissue expression of decorin and
lumican in embryonic quail cornea.";
Matrix Biol. 19:699-704(2000).
-:- FUNCTION: May affect the rate of fibrils formation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROFEOGLYCANS (SLRPS) FAMILY. CLASS I SUBFAMILY.
-!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
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SMART; SM00013; LRRT1; 1.
SMART; SM0016; LRR TYP; 7.
Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Decorin precursor (Bone proteoglycan II) (PG-S2).
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AF125250; AAC48154.1; ...
InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Nterm.
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InterPro; IPR003591; LRR_typ.
Pfam; PF00560; LRR; 10.
Pfam; PF01462; LRRNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352 TFACVTDRLAIQFGNY 367
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61 PRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEND 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 KVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGLP 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNK 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ::|||| | ||:||||||| LVRVPSGLGEHKXIQVVYLHNNKIASIGINDFCPLGYNTKRATYSGVSLFSNPVQYWEIQ 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQ 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDDTRE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                             O-LINKED (GLYCOSAMINOGLYCAN) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 974; DB 1; Length 356; Pred. No. 2.1e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LINKED (GLCNAC. . .) (POBE9583C6AED7DB26 CRC64;
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01-DEC-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Decorin precursor (Bone proteoglycan II) (PG-S2).
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67; Mismatches
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BY SIMILARITY.
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                        POTENTIAL.
                                                                                               CYS-RICH.
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LRR-T 1.
LRR-T 2.
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LRR-S 3.
LRR-T 5.
LRR-T 6.
LRR-S 4.
LRR-T 7.
LRR-T 8.
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LRR-T
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338 PSAFRCIHERSAVQIGNY 355
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  Leucine-rich repeat;
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P28675;
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                                                                                                                                              -:- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
-:- PTM: The attached glycosaminoglycan chain can be either chondroitin sulfate or dermatan sulfate depending upon the tissue of origin (By similarity).
-:- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SLRPS) FAMILY. CLASS I SUBFAMILY.
-:- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
                                                                                                           SUBUNIT: Binds to type I and type II collagen, to fibronectin and TGF-beta. Forms a ternary complex with MFAP2 and ELN (By
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N-LINKED (GLCNAC. .) (POTENTIAL).
31B104c7c3cD711D CRC64;
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R InterPro; IPR001611; I.RR.
R InterPro; IPR001622; I.RR_Nterm.
R InterPro; IPR001622; I.RR_Nterm.
R InterPro; IPR001622; I.RR_Nterm.
R Pfam; PP001660; I.RR, 8.
R Pfam; PP001660; I.RR, 1.
R SMART; SM00370; I.RR, 1.
R SMART; SM001370; I.RR, 1.
R SMART; SM00130; I.RR, 1.
R SMART; SM00130; I.RR_TYP; 2.
R Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
R SIGNAL.
I 1 16
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STRAIN=White leghorn; TISSUE=Cornea;

MEDLINE=22296755; PubMed=1605630;

Li W., Vergnes J.-P., Cornuet P.K., Hassell J.R.;

"CDNA clone to chick corneal chondroitin/dermatan sulfate

porteoglycan reveals identity to decorin.";

Arch. Biochem. Biophys. 296:199(-197(1992).

-i- FUNCTION: May affect the rate of fibrils formation (By
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LRR-S 1.
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LRR-T 2.
LRR-S 2.
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LRR-T 3.
LRR-T 4.
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LRR-T 5.
LRR-T 6.
LRR-T 6.
LRR-T 7.
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SUBCELLULAR LOCATION: Extracellular matrix (By similarity).

ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a short form; are produced by alternative splitcing.

PTM: The attached glycosaminoglycan chain can be either chondroitin sulfate or dermatan sulfate depending upon the tissue
                                                                                                                                                                                                                                                                                                                                                               47 GFG----PVCPFRCQCHLRVVQCSDLGLERVPKDLPPDTTLLDLQNNKITEIKEGDFKNL 102
                                                                                                                                                                                                  185 IQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGLPPTLL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 ELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKI 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 PSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATF 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223 ELHLDGNKISKIDAEGLSGLTNLAKLGLSFNSISSVENGSLNNVPHLRELHLNNNELVRV 282
65 FFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL 124
                                                                                                                                                         125 TSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metázoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROFEOGLYCANS (SIRPS) FAMILY. CLASS I SUBFAMILY.
SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-YOKSHIE; TISSUE-AOTE; Stephenson S., Schnoke M., Vesely I.; Stephenson S., Schnoke M., Vesely I.; Statematively spliced version of the porcine decorin gene."; Submitted (APR-1999) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stephenson S., Schnoke M., Vesely I.; "Cloning of the porcine decorin gene."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09XSD9; 09XSH4;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-UMV-2002 (Rel. 41, Last annotation update)
Decorin precursor (Bone proteoglycan II) (PG-S2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (LONG ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||: | :||:||:
343 RCIHERSAVQIGNY 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 RCVLSRMSVQLGNF 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (Pig).
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221 PPSLTELHLDGNKISKVDAASLKGLNNLAKLGLGFNSISTVDNGSLANTPHLRELHLNNN 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENN 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 EP-----LGPMCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTALLDLQNNKITEIKDG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 DFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
MISSING (IN SHORT ISOFORM).
8573DE8DDEBA7509 CRC64;
                                                                                                                                                                                                                                                                                                                                                 O-LINKED (GLYCOSAMINOGLYCAN) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 360;
                                                                             SMART; SM001370; LRR; 1.
SMART; SM000370; LRR; 1.
SMART; SM000159; LRR_TYP; 2.
SMART; SM00369; LRR_TYP; 2.
SMART; SM00369; LRR_TYP; 2.
SMART; SM00369; LRR_TYP; 3.
SMART; SM00369; LRR_TYP; 1.
SMART; SM00369; LRR_TYP; 1.
In 16
POTENTIAL.
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                                                                                                                                                         BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              63; Mismatches
                                                                                                                                                                                                                                                                                                                             BY SIMILARITY. BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                             SIMILARITY)
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LRR-T 1.
LRR-T 2.
LRR-T 3.
LRR-T 4.
LRR-S 3.
LRR-S 3.
LRR-S 5.
LRR-T 6.
LRR-T 6.
LRR-T 7.
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                                 LRR_Nterm.
EMBL; AF125537; AAD23578.1; -.
          AAD33862.1; -.
                                          InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
Pfam; PF00560; LRR: 7
Pfam; PF01462; LRRNT; 1.
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341 QPSTFRCVYVRSAIQLGNY 359
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          EMBL; AF140270; AAD33862.1
InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_N
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360
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94
118
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318
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304 3
281 3
360 AA;
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VARSPLIC
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RESULT 14

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similarity).
--- SUBCELLULAR LOCATION: Extracellular matrix.
--- ALTERNATIVE PRODUCTS: 5 isoforms; A (shown here), B, C, D and E; are produced by alternative splicing.
--- PIM: The attached glycosaminoglycan chain can be either chondroitin sulfate or dermatan sulfate depending upon the tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fisher L.W., Hawkins G.R., Tuross N., Termine J.D.;
Foone staloproteins I and II, and osteonectin from the mineral compartment of developing human bone.";
J. Bold. Chem. 262:9702-9708(1987).
J. Bold. Chem. 262:9702-9708(1987).
J. FINCTION: May affect the rate of fibrils formation.
J. SUBUNIT: Binds to type I and type II collagen, to fibronectin and TGF-beta. Forms a ternary complex with MFAP2 and ELN (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Danielson K.G., Fazzio A., Cohen I.R., Cannizzaro L., Iozzo R.V., "The human decorin gene: intron exon organization, discovery of two alternatively spliced exons in the 5' untranslated region, and mapping of the gene to chromosome 12q23."; Genomics 15:146-160(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roughley P.J., White R.J.; Roughley P.J. White R.J.; Permatan sulphate protections of human articular cartilage. The properties of dermatan sulphate proteoglycans I and II."; Biochem. J. 262:823-827(1989).
                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                               MEDLINE-87017013; PubMed-3484330;
Krustus T., Ruoslahti E.;
"Primary structure of an extracellular matrix proteoglycan core
protein deduced from cloned cDNA.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Vetter U., Vogel W., Just W., Young M.F., Fisher L.W.; "Human decorin gene: intron-exon junctions and chromosomal localization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS A; B; C; D AND E).
Cs. Szabo G., Glant T.T.;
"Alternative splicing of human decorin.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
PGS2_HUMAN STANDARD; PRT; 359 AA. P07585; Q9Y5N9; Q9Y5N8; Q9P0Z0; Q9P0Z1; C01-APR-1988 (Rel. 07, Created) 01-APR-1988 (Rel. 07, Last sequence update) 15-UNN-2002 (Rel. 41, Last annotation update) Decorin precursor (Bone proteoglycan II) (PG-S2) (PG40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SLRPS) FAMILY. CLASS I SUBFAMILY. SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR)
                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 83:7683-7687(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-70 FROM N.A. MEDLINE=93162642; PubMed=8432526;
                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Lung;
MEDLINE=93162643; PubMed=8432527;
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                                                                                                                                              Homo sapiens (Human).
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                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISSING (IN ISOFORM B).
MISSING (IN ISOFORM C).
MISSING (IN ISOFORM D).
LDKV -> CLPS (IN ISOFORM E).
MISSING (IN ISOFORM E).
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/FIId=VAR_011975.
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D -> P (IN REF. 7).
                                                                                                                            EMBL; L01127; AAA52301.1; JOINED.
EMBL; L01129; AAA52301.1; JOINED.
EMBL; L01130; AAA52301.1; JOINED.
EMBL; H0130; AAA52301.1; JOINED.
EMBL; AF138300; AAD44713.1; ---
EMBL; AF138301; AAF61437.1; ---
EMBL; AF138301; AAF61438.1; ---
EMBL; AF138304; AAD44715.1; ---
EMBL; AF138304; AAD44715.1; ---
EMBL; BC06532; AAH05322.1; ---
                                                                                   EMBL; M14219; AAB00774.1; -...EMBL; L01131; AAA52301.1; ALT_SEQ.EMBL; L01125; AAA52301.1; JOINED.EMBL; L01126; AAA52301.1; JOINED.
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InterPro; IPR000372; LRR_Nterm.
InterPro; IPR0003592; LRR_out.
InterPro; IPR003591; LRR_typ.
Pfam; PF00560; LRR; 7.
Pfam; PF01462; LRRNT; 1.
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SMART; SM00013; LRRNT; 1.
SMART; SM0369; LRR_TYP; 1.
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PIR; B28457; B28457.
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InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Nterm.
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                                     EMBL; AF125041; AAF00585.1; -.
                                                                                       InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
Pfam; PF00560; LRR; 9.
Pfam; PF01462; LRRNT; 1.
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360 AA;
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CARBOHYD
SEQUENCE
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                           4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use, by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s its content is in no way Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20113292; PubMed=10644528; Wu W.X., Zhang Q., Unno N., Derks J.B., Nathanielsz P.W.; "Characterization of decorin mRNA in pregnant intrauterine tissues of the ewe and regulation by steroids."; Am. J. Physiol. 278:C199-C206(2000).
                                                                                                                                                                                                                         220 PPSLTELHLDGNKISRVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHLKELHLDNN 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: The attached glycosaminoglycan chain can be either chondroitin sulfate or dermatan sulfate depending upon the tissue
                                                                                                     60 EPRSHFFFFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEN 119
                                                                                                                                                                      299 KLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEM 358
                                                                                                                                                                                                                                                                                                                              SUBUNIT: Binds to type I and type II collagen, to fibronectin and TGF-beta. Forms a ternary complex with MFAP2 and ELN (By
                                                                                                                                                        120 DFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHE 179
                                                                                                                    -----FEPSLGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNNKITEIKDG 99
                           Gaps
                                                                   1 MKEYVLLLFLALCS-AKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDSDNSLFPTR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                              239 PPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENN
                                                                                                                                                                                                           180 NKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of origin (By similarity).
SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SLRPS) FAMILY. CLASS I SUBFAMILY.
SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
48.4%; Score 963.5; DB 1; Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: May affect the rate of fibrils formation (By
                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Decorin precursor (Bone proteoglycan II) (PG-S2) (PG40).
          .le-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed.
          Pred. No. 1.1e
65; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   359 QPATFRCVLSRMSVQLGNF 377
                                                                                                                                                                                                                                                                                                                                                                                 340 QPSTFRCVYVRSAIQLGNY 358
         50.48;
                          191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FISSUE=Myometrium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGS2_SHEEP
Query Match
             Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                              PGS2_SHEEP
                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 KDGDFKNLKNLHTLILINNKISKISPGAFAPLVKLERLYLSKNQLKELPEKMPKTLQELR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 IHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVP 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 KGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 ENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKY 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 KENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKATIIFFLVAQVSWAGPF---QQKGLFDFML---------EDEASGIGP-- 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKEYVLLLFLALCS-AKPFFSPSHIALKNWMLKDMEDTDDDDDDDDDDDDDDDDDDDDDTFPTR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 QGLPPSLTELHLDGNKITKVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHLRELHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 VHENEITKVRKSVFNGLNQMIVVELGTNPLKSSGIENGAFQGMKKLSYIRIADTNITTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).

N.LINKED (GLCNAC. ) (POTENTIAL).

N.LINKED (GLCNAC. ) (POTENTIAL).

N.LINKED (GLCNAC. ) (POTENTIAL).

0095DODPDAB88624 CRC64;
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BY SIMILARITY.

O-LINKED (GLYCOSAMINOGLYCAN) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97; Indels
                                                                                                                                                                                                                                                                        SMART; SM00370; LRR; 2.
SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_TYP; 2.
Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
Leucine-rich repeat; Signal.
SIGNAL 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.5%; Score 947; DB 1; 49.7%; Pred. No. 1.6e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYS-RICH.
LRR-9 1.
LRR-7 2.
LRR-7 2.
LRR-7 3.
LRR-7 4.
LRR-7 4.
LRR-7 5.
LRR-7 5.
LRR-7 6.
LRR-7 6.
LRR-7 6.
LRR-7 6.
LRR-7 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DECORIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Characterization of the dermatan sulfate proteoglycans, DS-PGI and DS-FGII, from bovine articular cartilage and skin isolated by octylsephase chromatography."
J. Biol. Chem. 264:2876-2884(1989).
                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SLRPS) FAMILY. CLASS I SUBFAMILY.
-1- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-88133946; PubMed=3435485;
Day A.A., McQuillan C.I., Termine J.D., Young M.R.;
"Molecular cloining and sequence analysis of the cDNA for small proteoglycan II of bovine bone.";
Biochem. J. 248:801-805(1987).
                                                                                                                                                                                                                                                                                                SEQUENCE OF 31-54.
MEDLINE-89123388; PubMed-2914936;
Chol H.U., Johnson T.L., Pal S., Tang L.H., Rosenberg L.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SN00370, LRR; 2.
SMART; SN000370, LRR, 1.
SMART; SN00369; LRR_TYP; 2.
Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
Leucine-rich repeat; Signal.
SIGNAL 16
                                           01-MAY-1991 (Rel. 18, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Decorin precursor (Bone proteoglycan II) (PG-S2).
   360 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR001611; LRR.
Interpro; IPR001611; LRR_Nterm.
Interpro; IPR0018592; LRR_out.
Interpro; IPR0018591; LRR_cut.
Pfam; PF00560; LRR; 8.
Pfam; PF01462; LRRMT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERACTIONS WITH MFAP2 AND ELN.
                          01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequ
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Y00712; CAA68702.1; -.
 STANDARD;
                                                                                                                                                Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S06280; S06280.
B31430; B31430.
                                                                                                      taurus (Bovine).
                                                                                                                                                                 NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=11723132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of origin.
                                                                                                                                                                                                                                                                                                                                                Neame P.J.;
PGS2_BOVIN
P21793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR;
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60 EPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEN 119
                                                                                                                                                                                                                                                                                                                                                     120 DFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                239 PPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENN 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                 221 PPSLTELHLDGNKITKVDAASLKGLNNLAKLGLSFNSISAVDNGSLANTPHLRELHLNNN 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 KLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEM 358
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                           1 MKEYVLLLFLALCS-AKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDFDNSLFPTR 59
                                                                                                                                                                                                                                                                                      180 NKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                  N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                  O-LINKED (GLYCOSAMINOGLYCAN) (BY
                                                                                                                                                                                                                                    47.3%; Score 943; DB 1; Length 360; 49.1%; Pred. No. 3e-58;
                                                                                                                                                                                                                                                       69; Mismatches 102; Indels
                                                                                                                                                                                                                71E84DA2D87552C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGS2_RABIT STANDARD; PRT; 360 AA. Q28888; Q28608; 115-JUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Decorin precursor (Bone proteoglycan II) (PG-S2).
                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                            SIMILARITY)
        DECORIN.
CYS-RICH.
LRR-T 1 1.
LRR-T 2 1.
LRR-T 2 2.
LRR-T 3 2.
LRR-T 4 3.
LRR-T 4 3.
LRR-T 5 1.
LRR-T 5 1.
LRR-T 6 1.
LRR-T 6 1.
LRR-T 7 1.
LRR-T 7 1.
                                                                                                                                                                                                                 39837 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           359 QPATFRCVLSRMSVQLGNF 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341 QPSTFRCVYVRAAVOLGNY 359
                                                                                                                                                                                                                                              49.18;
                                                                                                                                                                                                                                                       Matches 186; Conservative
212
263
263
304
360 AA;
                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
NCB1_TaxID=9986;
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                                                                                                                                              DISULFID
                                                                                                                                                        DISULFID
                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                    CARBOHYD
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                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                               PTM: The attached glycosaminoglycan chain can be either chondroitin sulfate or dermatan sulfate depending upon the tissue of origin (By similarity).

SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SIRPS) FAMILY. CLASS I SUBFAMILY.

SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                  -1- SUBUNIT: Binds to type I and type II collagen, to fibronectin and TGF-beta. Forms a ternary complex with MFAP2 and ELN (By
                                                                                             Hering T.M., Kollar J.;
"The primary structure of rabbit chondrocyte decorin deduced from
nucleotide sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
           zhan Q., Burrows R., Cintron C.;
"Cloning and in situ hybridization of rabbit decorin in corneal
                                                                                                                                                                                                     SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O-LINKED (GLYCOSAMINOGLYCAN) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 360;
                                                                                                                                Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR001611; LRR.
Interpro; IPR000352; LRR. Nterm.
Interpro; IPR003592; LRR_out.
Interpro; IPR003591; LRR_typ.
Interpro; IPR003591; LRR_typ.
Pfam; PF00560; LRR; 7.
Pfam; PF00462; LRRH; 1.
SMART; SM00370; LRR; 1.
SMART; SM0013; LRRHT; 1.
SMART; SM0013; LRRTY; 1.
Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0B50C6756FE02369 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 941; DB 1;
Pred. No. 4.1e-58;
                                              Invest. Ophthalmol. Vis. Sci. 36:206-215(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY. DECORIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY.
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BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRR-T 2.
LRR-S 2.
LRR-T 3.
LRR-S 3.
LRR-T 5.
LRR-T 6.
LRR-T 6.
LRR-T 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JRR-S 1.
MEDLINE=95122319; PubMed=7822148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39896 MW;
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; S76584; AAB33083.1; -. EMBL; U03394; AAC04315.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.28;
                                                                      SEQUENCE OF 38-358 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360
68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212
263
304
360 AA;
                                                                                  TISSUE=Cartilage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity)
                                                                                                                                                        similarity)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                    tissues.
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Local Similarity

Best

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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Richardson D.W., Dodge G.R.; "Effects of interleukin-1 beta and tumor necrosis factor-alpha on the expression of matrix related genes in cultured equine articular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBBUNIT: Binds to type I and type II collagen, to fibronectin and TGF-beta. Forms a ternary complex with MFAP2 and ELN (By SUBLIBLINIAR LOCATION: Extracellular matrix (By similarity).

PTM: The attached glycosaminoglycan chain can be either
                                                                                                                                                                                                                                                                                                                                                                                                                          chondroitin sulfate or dermatan sulfate depending upon the tissue
                                                                                                                                                            180 NKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGL 238
                                                                                                                                   EPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEN 119
                                              1 MKEYVLLLFLALCS-AKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDTFPTR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Decorin precursor (Bone proteoglycan II) (PG-S2) (Dermatan sulfate Droteoglycan II) (DS-PGII).
                                                                                                                                                                                                                                                                                                                                       120 DFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHE
                                                                                                                                                                                                                                                                                                                                                                                                     239 PPILLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 KLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEM
                                                                                     1 MTATLILLLLAQVSWAGPF---QQRGLFDFMLED-EASGIGPDERAPELPDLDM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of origin (By similarity).
--- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SIRRS) FAMILY. CLASS I SUBFAMILY.
--- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chondrocytes.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: May affect the rate of fibrils formation (By
    67; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341 QPSTFRCVYMRSAIQLGNY 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359 OPATFRCVLSRMSVQLGNF 377
    Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 PPGEPPSLTELHLDGNKITKVDDASERGLNNLAKLGESFNSISAVDNGSLANTPHLRELH 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 IKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAEL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 PKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIH 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295 LENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVK 354
                                                                                                                                                                                                                                                                                                                                                                                             97; Indels 30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             39 EDRIHEVLDLEP--LGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNNKITE 96
                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
2DAE97CDE16F7C45 CRC64;
                                                                                                                                                                                                                                                                                                      O-LINKED (GLYCOSAMINOGLYCAN) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                    (GLYCOSAMINOGLYCAN) (BY
                                                                                                                                                                                                                                                                                                                                                                        47.1%; Score 939; DB 1; Length 360;
49.3%; Pred. No. 5.7e-58;
tive 67; Mismatches 97; Indels
                                                                              Glycoprotein; Extracellular matrix; Proteoglycan; Repeat; Leucine-rich repeat; Signal.
                                                                                                                                                                                                                                                     LRR-T 8.
BY SIMILARITY.
BY SIMILARITY.
O-LINKED (GLYCO
                                                                                                             BY SIMILARITY.
DECORIN.
                                                                                                                                                                                                                                                                                               SIMILARITY)
                                                                                                  POTENTIAL
                                                                                                                                  CYS-RICH.
                                                                                                                                          LRR-S 1.
LRR-T 1.
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LRR-S 3.
LRR-T 5.
LRR-T 6.
LRR-T 6.
LRR-S 4.
                                                                                                                                                                        LRR-S
EMBL; AF038127; AAB92652.1; -.
InterPro; IPR001611; LRR.
InterPro; IPR00372; LRR_Nterm.
InterPro; IPR003592; LRR_out.
Pfam; PF00460; LRR; 8.
SMART; SM00370; LRR.; 1.
SMART; SM00013; LRRNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         337 YWEIQPSTFRCVYVRSAIQLGNY 359
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                                                                                                                                                                                                                                                                                                                          212
263
304
39939 MW;
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30
360
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118
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1163
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PGS2_CANFA
ID PGS2_CANFA
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                                                                                                  SIGNAL
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360 AA.

PRT;

STANDARD;

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                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
-!- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
TGF-beta. Forms a ternary complex with MFAP2 and ELN (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: The attached glycosaminoglycan chain can be either chondroitin sulfate or dermatan sulfate depending upon the tissue
                                                                                                                      Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                               SEQUENCE OF 244-259 FROM N.A. Venta P.J., Brower G.J.; Venta P.J., Brouillette J.A., Yuzbasiyan-Gurkan V., Brewer G.J.; Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of origin (By similarity).
SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SLRPS) FAMILY.
CLRAS I SUBFAMILY.
SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O-LINKED (GLYCOSAMINOGLYCAN) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; PR001011; LRR.
InterPro; PR001011; LRR.
InterPro; IPR000372; LRR.
InterPro; IPR003592; LRR.
InterPro; IPR003592; LRR.
InterPro; IPR003591; LRR.
InterPro; IPR003591; LRR.
InterPro; IPR003591; LRR.
InterPro; IPR003591; LRR.; J.
SMART; SM00370; LRR; J.
SMART; SM00369; LRR.; J.
Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
Leucine-rich repeat; Signal.
SIGNAL.
InterPro; IRR.
I
                                                                                                                                                                                                                                                                         Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases
             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Decorin precursor (Bone proteoglycan II) (PG-S2).
DCN OR DCNIC.
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DECORIN.
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BY SIMILARITY.
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LKR-T 1.
LKR-T 2.
LKR-S 2.
LKR-G 3.
LKR-T 4.
LKR-T 4.
LKR-S 3.
LKR-T 6.
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LRR-T 7.
LRR-T 8.
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347
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                      NCBI_TaxID=9615;
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SUBCELLURAR LOCATION: Extracellular matrix.
PUR. The attached glycosaminoglycan chain can be either chondroitin sulfate or dermatan sulfate depending upon the tissue
                                                                                                                                                                                                                                           -----LLGPVCPFRCQCHLRVVQCSDLGLDKVPKDLPPDTTLLDLQNNKITEIKDG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEM 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 KLIRVPGGLAEHKYIQVVYLHNNNISAVGSNDFCPPGYNTKKASYSGVSLFSNPVQYWEI 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                        60 EPRSHFFFFFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKEN 119
                                                                                                                                                                                                                                                                                                DFKGLTSLYGLILUNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHE 179
                                                                                                              Gaps
                                                                                                                                                                                   49
                                                                                                                                                 1 MKEYVLLLFLALCS-AKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDSDNSLFPTR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosomal assignment, and expression during organogenesis and tissue differentiation.":

Biol. Chem. 269:28270-28281(1994).

-!- FUNCTION: May affect the rate of fibrils formation.

-!- SUBUNIT: Binds to type I and type II collagen, to fibronectin TGF-beta. Forms a ternary complex with MFAP2 and ELN (By
                                                                                                                                                                                                                                                                                                                     PPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   221 PPSLTELHLEGNKITKVDASSLKGLNNLAKLGLSFNSISAVDNGTLANTPHLRELHLDNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus
                                                                                                                                                                                   1 MKATIIFLLLAQVSWAGPF --- QQRGLFDFMLEDEASGIGPEDRAPDMPDLE -----
                                                                                                                                                                                                                                                                                                                                                                         NKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

BEDLINE-95050610; PubMed-7961765;
Scholzen T., Solursh M., Suzuki S., Reiter R., Morgan J.L.,
Scholzen T., Siracusa L.D., Iozzo R.V.;
Buchberg A.M., Siracusa L.D., Iozzo R.V.;
"The murine decorin. Complete CDNA cloning, genomic organization,
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
99BEE11A9C812906 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of origin (By similarity).
SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
                                                                     Length 360;
                                                                                                            67; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Decorin precursor (Bone proteoglycan II) (PG-S2) (PG40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Naitoh Y., Suzuki S.;
Submitted (JUL-1990) to the EMBL/GenBank/DDBJ databases.
                                                                       DB 1;
                                                                                        1.3e-57
                                                                       46.9%; Score 934;
                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-NIH Swiss; TISSUE-Fibroblast;
Naitch Y., Suzuki S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
263
304
39980 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPATFRCVLSRMSVQLGNF 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341 QPSTFRCVYVRSAIQLGNY 359
                                                                                        49.18;
                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         musculus (Mouse)
                                    360 AA;
                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGS2_MOUSE
                                                                                                            186;
CARBOHYD
                 CARBOHYD
                                    SEQUENCE
                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28654;
                                                                                            Best Local
                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                    101
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMIL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 LOELRVHENEITKLRKSDFNGLNNVLVIELGGNPLKNSGIENGAFOGLKSLSYIRISDTN 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REIHLENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFN 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 KIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 FPTREPRSHFFPFD----LFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNN 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FMLEDEASGIIPYDPDNPLISMCPYRCQCHLRVVQCSDLGLDKVPWDFPPDTTLLDLQNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 LAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRR-T 1.

LRR-T 2.

LRR-T 3.

LRR-T 4.

LRR-S 3.

LRR-S 3.

LRR-S 4.

LRR-T 6.

LRR-T 7.

LRR-T 7.

LRR-T 7.

LRR-T 7.

LRR-T 7.

LRR-T 8.

LRR-T 9.

LRR-T 9.

LRR-T 10.

LRR-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.6%; Score 907.5; DB 1; Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                  Prom. PF01462; LRRNT; 1.
SMART; SM00370; LRR; 2.
SMART; SM00013; LRR_TVP; 2.
Glycoprotein; Extracellular matrix; Proteoglycan; Repeat; Leucine-rich repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87; Indels
(SLRPS) FAMILY. CLASS I SUBFAMILY. SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F05B5CC08DCABF6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 8.3e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65; Mismatches
                                                                                                                                                                                                                                                                                                                                                    LRR_Nterm.
                                                                                                                                                                                                                                                                                                                                                                           LRR_out.
LRR_typ.
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                                                                                                                                                                                                                                                            PIR; S20812; S20812.
HSSP; P23945; IXUN.
MGD; MGI:94872; DGN.
InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_N
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88
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InterPro; IPR003591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
257
298
354 AA;
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  Óλ
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similarity).
SUBCELLULAR LOCATION: Extracellular matrix.
DEVELOPMENTAL STAGE: The amount of DSPG per cervix increases 4-fold during pregnancy, then falls precipitously within 1 day post
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FMR: The attached glycosaminoglycan chain can be either chondroitin sulfate or dermatan sulfate depending upon the tissue of origin (By similarity).

SIMILABITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SLRPS) FAMILY. CLASS I SUBFAMILY.

SIMILABITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fibronectin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Abramson S.R., Woessner J.F., "cDNA sequence for rat dermatan sulfate proteoglycan-II (decorin)."; Biochim. Biophys. Acta 1132:225-227(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Asundi V.K., Dreher K.L.;
"Molecular characterization of vascular smooth muscle decorin:
deduced core protein structure and regulation of gene expression.";
Eur. J. Cell Biol. 59:314-321(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Last annotation update)
Decorin precursor (Bone proteoglycan II) (PG-S2) (PG40) (Dermatan sulfate proteoglycan-II) (DSPG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Purification and characterization of a small dermatan sulphate proteoglycan implicated in the dilatation of the rat uterine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. J. 260:413-419(1989).
-!- FUNCTION: May affect the rate of fibrils formation (By similarity). May be implicated in the dilatation of the rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: Binds to type I and type II collagen, to fibron TGF-beta. Forms a ternary complex with MFAP2 and ELN (By
                                                                                                                                                                                                                                                                                                                                      354 AA
                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Sprague-Dawley; TISSUE=Uterus; MEDLINE=93003331; PubMed=1390895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [3] SEQUENCE OF 31-48 AND 171-191.
SEQUENCE OF 31-8 AND 171-191.
STRAIN=Sprague-Dawley; TISSUE-Uterus;
MEDLINE-89350825; PubMed=2764879;
                                                                                                    351 NPVKYWEMQPATFRCVLSRMSVQLGNF 377
                                                                                                                                                               327 NPVRYWEIFPNTFRCVYVRSAIQLGNY 353
                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kokenyesi R., Woessner J.F., "Purification and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 11-354 FROM N.A.
MEDLINE=93154359; PubMed=1493796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z12298; CAA78170.1; -.
                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1993
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                   PGS2_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cervix."
                                                                                                                                                                                                                                                                    RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         + +
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60 EPRSHFFPFD----LFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 IKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAEL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 RIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVT-VFHIRIAEAKLTSV 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 LENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVK 354
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKEYVLLIFLALCS-AKPFFSPSHIALKNWMLKDMEDTDDDDDDDDDDDDDDDDDDDDDFPTR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .----- 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLONAC. .) (POTENTIAL)
N-LINKED (GLONAC. .) (POTENTIAL)
152D92F42D9F5A5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              36;
                                                                                                                                                                                                                                                                                                                        O-LINKED (GLYCOSAMINOGLYCAN) (BY
                                                                                       M Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;

M Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;

SIGNAL 1 16 POTENTIAL.

T CHAIN 31, 354 DECORIN.

T CHAIN 49, 62 CYS.RICH.

T REPEAT 68 88 LRR-5 1.

REPEAT 113 136 LRR-7 1.

REPEAT 113 136 LRR-7 2.

T REPEAT 159 181 LRR-7 2.

T REPEAT 182 207 LRR-7 3.

REPEAT 208 228 LRR-7 3.

REPEAT 208 228 LRR-5 3.
                                                                                                                                                                                                                                                                                                     O-LINKED (GLYCOSAMINOGLYCAN) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                              99; Indels
                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.1%; Score 899; DB 1; 46.5%; Pred. No. 3.2e-55;
                                                                                                                                                                                                                                                                              SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                             70; Mismatches
                                                                                                                                                                                                                                                                                BY SIMILARITY BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
                                                                                                                                                                                                                                                                                                                SIMILARITY
                                                                                                                                                                 LRR-T 1.
LRR-T 2.
LRR-T 3.
LRR-T 3.
LRR-T 4.
LRR-S 3.
LRR-T 5.
LRR-T 5.
LRR-T 6.
LRR-T 7.
LRR-T 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355 YWEMQPATFRCVLSRMSVQLGNF 377
          LRR_Nterm.
                 InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
                                                                                                                                                                                                                                                                                                                                                                                    39805 MW;
                                      Pfam; PF00560; LRR; 8.
Pfam; PF01462; LRRNT; 1.
SMART; SM00370; LRR; 2.
SMART; SM00013; LRRP; 1.
SMART; SM00013; LRRP; 1.
 IPR001611; LRR.
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           IPR000372;
                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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241
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298
354 AA;
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348
                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 178;
  InterPro;
          InterPro;
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RESULT 22

EMBL; X59859; CAA42519.1; -. PIR; S29145; S29145.

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                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- TISSUE SPECIFICITY: Found in several connective tissues, specially in articular cartilages.
-:- PTM: The two attached glycosaminoglycan chains can be either chondroitin sulfate or dermatan sulfate (By similarity).
-:- SIMILARITY: BELOWGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SLRPS) FAMILY. CLASS I SUBFAMILY.
-:- SIMILARITY: CONTAINS AT LEAST 9 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                  Eukaryota; Metázoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By similarity).
-i- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O-LINKED (GLYCOSAMINOGLYCAN) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O-LINKED (GLYCOSAMINOGLYCAN) (BY
                                                                                                                                                                                                                                                                                                                                       "Cloning and sequencing of porcine matrix molecules.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May be involved in collagen fiber assembly (By
                   09GKG6: 09TTB5;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
BiglyCan precursor (Bone/Cartilage proteoglycan I) (PG-SI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein; Extracellular matrix; Proteoglycan; Repeat; Leucine-rich repeat; Signal.
                                                                                                                                                                                                                                                                                                                     Wang J.F., Boykiw R.H., Reno C.R., Olson M.E., Hart D.A.;
                                                                                                                                                                                                                                                             Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases,
              272 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY. BIGLYCAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
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LRR-T 1.
LRR-T 2.
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LRR-S 3.
LRR-T 5.
LRR-T 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRR-S 4.
LRR-T 7.
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InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF054419; AAG39274.1; -. EMBL; AF159382; AAF19153.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003591; LRR_typ.
                                                                                                                                                                                                                                                                                            SEQUENCE OF 138-272 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01462; LRRNT; 1.
Pfam; PF00560; LRR; 4.
SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_TYP; 1.
                                                                                                                                                                                                                SEQUENCE OF 1-137 FROM N.A.
                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103
127
>137
                                                                                                                                      Sus scrofa (Pig).
                                                                                                                                                                                     NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                       similarity)
                                                                                                                                                                                                                                  rissue-Aorta;
                                                                                                                                                                                                                                                                                                            rissue-skin;
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                PGS1_PIG
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CHAIN
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PGS1_PIG
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                                                                                                                    5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- SUBCEDIOLAR LOCATION: Extracellular matrix (By similarity).
-:- TISSUE SPECIFICITY: Found in several connective tissues, specially in articular cartilages.
-:- FTM: The two attached glycosaminoglycan chains can be either chondroitin sulfate or dermatan sulfate (By similarity).
-:- SIMILARITY: BELONGS TO THE SMALL LEUGINE-RICH PROTEOGLYCANS (SLRPS) FAMILY. CLASS I SUBFAMILY.
-:- SIMILARITY: CONTAINS AT LEAST 6 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 PPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENN 298
                                                                                                                                                                                                                            59 REPRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKE 118
                                                                                                                                                                                                                                                                                                119 NDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIH 178
                                                                                                                                                       4 YVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDD-----DDDDDDDDDDDDDDDDFPT 58
                                                                                                                                                                               Boykiw R.H., Sciore P., Reno C.R., Marchuk L., Frank C., Hart D.A.; "Altered levels of extracellular matrix molecules mRNA in healing
                                                                                                                                                                                                                                                                                                                                                                      179 ENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                      90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 KLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNN 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Watrix Biol. 171.371.378(1998).
-!- FUNCTION: May be involved in collagen fiber assembly (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Biglycan (Bone/Cartilage proteoglycan 1) (PG-S1) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By
                                                                                 32.2%; Score 641; DB 1; Length 272; 39.1%; Pred. No. 1.5e-37;
                                                                                                                      73; Indels
              77 BY SIMILARITY.
272
30457 MW; GEBBADOEF86378BB CRC64;
                                                                                                                                                                                                                                                                                                                      PRT; 135 AA.
                                                                                                                      52; Mismatches
SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=New Zealand white;
MEDLINE=99037997; PubMed=9822203;
                                                                                                                        Conservative
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              64
272
272 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rabbit ligaments.";
Matrix Biol. 171:37
                                                                                                       Similarity
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                                                                                                                          138;
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046377;
              DISULFID
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SEQUENCE
                                                                                      Query Match
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"Identification of the N-linked oligosaccharide sites in chick corneal
lumican and keratocan that receive keratan sulfate.";
J. Biol. Chem. 273:9615-9621(1998).
-!- SUBUNIT: Binds to laminin (By similarity).
-!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
-!- TISSUE SPECIFICITY: Cornea and other tissues.
-!- PTM: Binds keratan sulfate chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 79-85; 155-167 AND 246-256, AND CARBOHYDRATE-LINKAGE SITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-92112674; PubMed-1370446; Blochberger T.C., Vergnes J.-P., Hempel J., Hassell J.R.; Conhort or corneal keratan sulfate proteoglycan) reveals homology to the small interstitial proteoglycan gene family and expression in muscle and intestine.";
                                                                                                                                                                                                                                                                                                                                                                                                             277 TDIENGSLANIPRVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVP 336
                                                                                                                                                                                                                                                                                                                                                     217 EGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKI 276
                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                  1 DGLKLNYLRISEAKLTGIPKDLPETLNELHLDHNKIQAIELEDLLRYSKLYRLGLGHNQI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lumican precursor (Keratan sulfate proteoglycan lumican) (KSPG
                                                                                                                                                                                                                                                                                            ; Score 442; DB 1; Length 135;
; Pred. No. 3.5e-24;
30; Mismatches 25; Indels
                                                                                                                 Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
Leucine-rich repeat.
                                                                                                                                                        343 AA
                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Cornea;
MEDLINE=98211990; PubMed=9545293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 267:347-352(1992).
                                          EMBL; AF020290; AAC39515.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 34, Created)
                                                       InterPro; IPR001611; LRR.
InterPro; IPR003591; LRR_typ.
                                                                                                                                                                                                                                                                                             22.2%;
59.3%;
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                                                                                    Pfam; PF00560; LRR; 5. SMART; SM00369; LRR_TYP; 1.
                                                                                                                                                                                                                                                                                                                         80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GVKRAYYNGISLENN 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337 KMKKSLYSAISLFNN 351
                                                                                                                                                                                                                                                                                                           Similarity
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01-OCT-1996
15-JUN-2002
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SEQUENCE
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م
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N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 EIKENDFKGLTSLYGLILNNNKL--TKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 DDLQLSHNKITKVNPGALEGLVNLTVIHLQNNQLKTDSIS-GAFKGLNSLLYLDLSFNQL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 REIHLENNKLKKIPSGLPELK--YLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISL 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 PFDLFPMCPFG------CQC---YSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 AIEENTFDNVTDLOWLILDHNHLENSKIKGRVFSKLKNLKKLHINYNNLTEAVGPLPKTL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 AELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232 TSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIE-NGSLANIPRV
SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SLRPS) FAMILY. CLASS II SUBFAMILY. SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.1%; Score 399.5; DB 1; Length 343; 31.9%; Pred. No. 9.6e-21; live 72; Mismatches 125; Indels 25
                                                                                                                                                                                                   Pfam; PF00560; LRR; 9.
Pfam; PF01462; LRRNT; 1.
PRINTS; PR00019; LEGRICHRPT.
SMART; SM00370; LRR; 1.
SMART; SM00370; LRR.; 1.
SMART; SM00369; LRR_TYP; 1.
Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
Leucine-rich repeat; Signal.
SIGNAL
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                               or send an email to license@isb-sib.ch).
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LRR-T 3.
LRR-T 4.
LRR-S 3.
LRR-T 5.
LRR-T 6.
LRR-T 6.
LRR-T 7.
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                                                                                                                                                                   InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38642 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 31.9%
Matches 104; Conservative
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257 2
320 3
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CARBOHYD
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                    Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
                                                                                                                                                                                                                                                                         Conrad G.W.;
                                                                                                                                                                                                                                                                         Corpuz L.M., Dunlevy J.R., Hassell J.R., Conrad A.H., Conrad G.W. "Molecular cloning and relative tissue expression of decorin and
                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lumican precursor (Keratan sulfate proteoglycan lumican) (KSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00019; LEURICHRPT.
SMART; SM00370; LRR; 4.
SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_TYP; 8.
Glycoproteal; Extracellular matrix; Proteoglycan; Repeat;
Leucine-rich repeat; Signal.
                                                                             343 AA.
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LRR-T 2.
LRR-T 3.
LRR-T 4.
LRR-T 3.
LRR-S 3.
LRR-T 5.
LRR-T 6.
LRR-T 7.
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                                                                            PRT;
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349 FNNPVKYWEMQPATFRCVLSRMSVQL 374
                     317 DGNNLTRADLPQEMYNCLRVAADISL 342
                                                                                                                                                                                                                                                             MEDLINE=20556471; PubMed=11102759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001611; LRR.
InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_Out.
InterPro; IPR003591; LRR_typ.
Pfam; PF00560; LRR; 9.
Pfam; PF01462; LRRNT; 1.
                                                                                                  (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF125251; AAG48155.1; -.
                                                                             STANDARD;
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201
222
246
271
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321
343
333
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                           NCBI_TaxID=93934;
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82
1106
1132
1177
1177
222
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332
300
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                                                                                                 15-JUN-2002
                                                                                                                                                           LUM OR LDC
                                                                             LUM_COTJA
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DISULFID
CARBOHYD
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                                                                   LUM_COTJA
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232 TSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIE-NGSLANIPRV 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 REIHLENNKLKKIPSGLPELK--YLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISL 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 VELDLSFNQLKSIPTVSENLENFYLQV-----NKINKFPLSSFCKVVGPLTYSKITHIRL 316
                      . .) (KERATAN SULFATE)
                                                                                  . .) (KERATAN SULFATE)
                                                                                                                                                                                                                                                                                                                                                                                                                       67 PFDLFPMCPFG------CQC---YSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 EIKENDFKGLTSLYGLILNNNKL--TKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 AELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 DDLQLSHNKITKVNPGALEGLVNLTVIHLQNNQLKADSIS-GAFKGLNSLLYLDLSFNQL 201
                                                                                                                                       . .) (KERATAN SULFATE)
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 PADDYGYDPFGPSTAVCAPECNCPLSYPTAMYCDNLKLKTIPI-VPSGIKYLYLRNNMIE 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Primary structure of human lumican (keratan sulfate proteoglycan) and localization of the gene (LUM) to chromosome 12q21.3-q22."; Genomics 27:481-488(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosomal location, and
                                                                                                                                                                                                       .) (POTENTIAL).
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15-JUN-2002 (Rel. 41, Last annotation update)
Lumican precursor (Keratan sulfate proteoglycan lumican) (KSPG
                                                                                                                                                                                                                                                                                               DB 1; Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chakravarti S., Stallings R.L., Sundarraj N., Cornuet P.K.,
                                                                                                                                                                                                                                                                                                                                                        125; Indels
                                                                                                                                                                                                   N-LINKED (GLCNAC. . .) (PO
A95199C7F32B7C4C CRC64;
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                      (GLCNAC.
                                                                                     (GLCNAC.
                                                                                                                                       N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                           31.9%; Pred. No. 1.1e-20; ive 72; Mismatches 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             338 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Cartilage, Intestine, and Placenta; MEDLINE-95394964; PubMed-7665616;
                                                                                                                                                                                                                                                                                               Score 398.5;
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(POTENTIAL).
                                                            (POTENTIAL).
                                                                                                                                                                             (POTENTIAL)
                                                                                                              (POTENTIAL)
                                                                                     N-LINKED
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J. Biol. Chem. 270:21942-21949(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349 FNNPVKYWEMQPATFRCVLSRMSVQL 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         317 DGNNLTRADLPOEMYNCLRVAAEISL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                         38642 MW;
                                                                                                                                                                                                                                                                                               20.0%;
                                                                                                                                                                                                                                                                                                                               al Similarity 31.9
104; Conservative
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                                                                                                                                                                                                                                         343 AA;
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                            130
                                                                                     165
                                                                                                                                              257
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                            CARBOHYD
                                                                                     CARBOHYD
                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                         SEQUENCE
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119 NDFKGLTSLYGLILNNNKL--TKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93280153; PubMed=8099356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_out.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L11063; AAA30608.1; -.
                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                    353 VKYWEMQPATFRCV 366
                                                                                                                                                                                                        316 ISETSLPPDMYECL 329
                                                                                                                                                                                                                                                                                                                                                                                Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                           IISSUE=Cornea;
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                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
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                                                                                                                    201
                                                                                                                                         295
                                                                                                                                                                                                                                         RESULT 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
      Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

-! SUBUNIT: Binds to laminin (By similarity).

-! SUBCELIULAR LOCATION: Extracellular matrix (By similarity).

-! TISSUE SPECIFICITY: Cornea and other tissues.

-! DEVELOPMENTAL STAGE: Present in the extracellular matrix of human articular cartilage at all ages, although its abundance is far greater in the adult in the adult cartilage lumican exists predominantly in a glycoprotein form lacking keratan sulfate, whereas the juvenile form of the molecule is a proteoglycan.

-! SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SLRPS) FAMILY: CLASS II SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 FPFDLF----PMCPFGCQC---YSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 FPLSIYGQSSPNCAPECNCPESYPSAMYCDELKLKSVPM-VPPGIKYLYLRUNQIDHIDE 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 338;
                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
Leucine-rich repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            905D2EBD370CC59D CRC64;
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-> V (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 4.2e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 390; DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CYS-RICH.
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LRR-T 1.
LRR-T 2.
LRR-S 2.
LRR-T 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRR-T 7.
LRR-T 8.
                                                                                                                                                                                                                                                                                                                                                                                                                        LUMICAN.
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LRR-T
LRR-T
LRR-S
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LRR-T
LRR-T
                                                                                                                                                                                                                                                                                        Interpro; IPR001611; LRR.
Interpro; IPR000372; LRR_Nterm.
Interpro; IPR003592; LRR_out.
Interpro; IPR003591; LRR_cut.
Pfam; PF00560; LRR; 9.
Pfam; PF00462; LRRNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38429 MW;
                                                                                                                                                                                                                              EMBL; U18728; AAA85268.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                    Signal.
18
                                                                                                                                                                                                                                              EMBL; U21128; AAA91639.1; -. EMBL; BC007038; AAH07038.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.8%;
                                                                                                                                                                                                                                                                                                                                                         SM00370; LRR; 4.
SM00013; LRRNT; 1.
SM00369; LRR_TYP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 100; Conservative
                                                                                                                                                                                                                                                                     Genew; HGNC:6724; LUM.
MIM; 600616; -.
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 Strausberg R.;
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                                                                                                                                                                                                                                                                                                                                                                    SMART;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
84 KAFENVTDLQWLILDHNLLENSKIKGRVFSKLKQLKKLHINHNNLTESVGPLPKSLEDLQ 143
                                                                                                                                                                                                                                           236 KGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIE-NGSLANIPRVREIH 294
                                                                                                                                                                                                                                                                                                                                                                                                        LENNKLKKIPSGLPELK--YLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNP 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                    IHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Funderburgh J.L., Funderburgh M.L., Brown S.J., Vergnes J.-P., Hassell J.R., Mann M.M., Conrad G.W.; "Sequence and structural implications of a bovine corneal keratan Sequence and structural prolection. Protein 37B represents bovine lumican and proteins 37A and 25 are unique."; J. Biol. Chem. 268:11874-11880(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KSPG) (Corneal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biol. Chem. 265:8297-8303(1990).
-!- SUBUNIT: Binds to laminin.
-!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- TISSUE SPECIFICITY: Cornea and other tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SLRPS) FAMILY. CLASS II SUBFAMILY.
-!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90243714; PubMed=2139877;
Funderburgh J.L., Conrad G.W.;
"Isoforms of corneal keratan sulfate proteoglycan.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0c7-1996 (Rel. 34, Created)
01-0C7-1996 (Rel. 34, Last sequence update)
115-JUN-2002 (Rel. 41, Last annotation update)
Lumican precursor (Keratan sulfate proteoglycan)
keratan sulfate proteoglycan 378 core protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342 AA.
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10;
                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 NDFKGLTSLYGLILUNNKL--TKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 IHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVP 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : ||: |: : : : : : | | : : | : : | : : : : : : : : : | 148 LINNKISKL--GSFDGLVNLTFIHLQHNQLKEDAVS-AALKGLKSLEYLDLSFNQMIKLP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENNKLKKIPSGLPELK -- YLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNP 352
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                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
                                                                                                                                                                                                                                                                                                                        . .) (KERATAN SULFATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 FPFDLF----PMCPFGCQC---YSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KAFENVTDLQWLILDHNLLENSKIKGKVFSKLKQLKKLHINYNNLTESVGPLPKSLVDLQ 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 KGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDI-ENGSLANIPRVREIH 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LUM_MOUSE STANDARD, PRT; 338 AA.
P51885; Q9CXK0; Q99J23;
O1-OCT-1996 (Rel. 34, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lumican precursor (Keratan sulfate proteoglycan lumican) (KSPG
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                           68; Mismatches 123; Indels
                                                           SMART; SM00369; LRR_TYP; 1.
Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
Leucine-rich repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                            592DEE9A489AEB79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 384; DB 1;
Pred. No. 1.1e-19;
                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                    BY SIMILARITY.
                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
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LRR.S. 1.

LRR.T. 2.

LRR.T. 3.

LRR.T. 3.

LRR.T. 4.

LRR.T. 3.

LRR.T. 5.

LRR.T. 5.

LRR.T. 5.

LRR.T. 6.

LRR.T. 6.

LRR.T. 6.

LRR.T. 7.
                                                                                                                                                                                                                                                                                                                                                                                           342 AA; 38756 MW;
Pfam; PF00560; LRR; 9.
Pfam; PF01462; LRRNT; 1.
PRINTS; PR00019; LEURICHRPT.
SMART; SM00370; LRR; 1.
SMART; SM00013; LRRNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   19.3%;
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63
83
1007
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 101;
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KRAIN-C57BL/G61. TISSUE-Embryonic head;

KRA Kawai J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

KA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

KA Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Psoule G., Quadkenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboddi M.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboddi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamcto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Hyashizaki Y., Toyo-oka K., Wang K.H., Weitz C., Whitttaker C., Wilming L.,

RA Hyashizaki Y., Soshida K., Hassegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y., Soshida K., Hassegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.ch).
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                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Yao C.W.-C., Converse R.L., Funderburgh J.L., Ying S., Shiraishi A., Kao W.W.-Y.; Swiergiel J., Roth M.R., Kao W.W.-Y.; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                       MEDLINE=96006258; PubMed=7558724; Mevelone N.D., Stech M.E., Justice M.J., Liu C.-Y., Kao W.W.-Y., Conrad G.W.; Liu C.-Y., Kao W.W.-Y., Conrad G.W.; Sequence, molecular properties, and chromosomal mapping of mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- SUBUNIT: Binds to laminin (By similarity).
-:- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
-:- TISSUE SPECIFICITY: Cornea and other tissues.
-:- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SLRPS) FAMILY. CLASS II SUBFAMILY.
-!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                            Invest. Ophthalmol. Vis. Sci. 36:2296-2303(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000372; LR.Nterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
Pfam; PP00560; LRR, 9.
Pfam; PF01462; LRRNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF013262; AAB87767.1; -. AK014312; BAB29264.1; -. BC005550; AAH05550.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:685-690(2001).
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                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Breast;
                                                                                                                                            TISSUE=Cornea;
                                                                                                                                                                                                                                                         lumican.
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160
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                                                                                [1]
SEQUENCE FROM N.A.
                                                                NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 TVNENLENYYLEV----NELEKFDVKSFCKILGPLSYSKIKHLRLDGNPLTQSSLPPDM 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 KDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGLPPTLLEL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGLPELK -- YLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPAT 362
                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (KERATAN SULFATE) (POTENTIAL).
N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 PMCPFGCQC---YSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 GLILINNNKL--TKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQ 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 HLDYNKISTVELEDFKRYKELQRLGLGNNKITDI-ENGSLANIPRVREIHLENNKLKKIP 304
                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
                                                                                                                                                                                                                                                                                                                                                                                   . .) (KERATAN SULFATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 PNCAPECNCPHSYPTAMYCDDLKLKSVPM-VPPGIKYLYLRNNQIDHIDEKAFENVTDLQ 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lumican precursor (Keratan sulfate proteoglycan lumican) (KSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 338;
             SMART; SM00370; LRR; 1.
SMART; SM00013; LRRNT; 1.
SMART; SM0369; LRR_TYP; 1.
Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
Leucine-rich repeat, Signal BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 19.2%; Score 383; DB 1; Length 33 Best Local Similarity 32.9%; Pred. No. 1.3e-19; Matches 100; Conservative 66; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> M (IN REF. 3).
-> E (IN REF. 1 AND 2).
-> T (IN REF. 1 AND 2).
FF1E050C89779140 CRC64;
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                                                                                            SIMILARITY
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(POTENTIAL)
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                                                                                                                         CYS-RICH.
LRR-S 1.
LRR-T 1.
LRR-T 2.
LRR-S 2.
LRR-S 2.
                                                                                                                                                                                                     LRR-T 3.
LRR-S 3.
LRR-T 5.
LRR-T 5.
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                                                                                                              LUMICAN
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LRR-S
LRR-T
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PRINTS; PR00019; LEURICHRPT
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109
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326 YECL 329
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CONFLICT
SEQUENCE
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P51886;
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NAME OF A PART O
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLFPMCPFGCQC----YSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLT 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBCNIT: Binds to laminin (By similarity).
-i- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
-i- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SLRPS) FAMILY. CLASS II SUBFAMILY.
-i- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X84039; CAA58858.1; -.
R InterPro; IPR001511; LRR.
R InterPro; IPR001522; LRR_cut.
R InterPro; IPR003522; LRR_cut.
R InterPro; IPR003521; LRR_LYP.
R Ffam; PF01462; LRRYT; 1.
R SAMRT; SM000137; LEURICHRPT.
SMART; SM00370; LRR; 1.
R SAMRT; SM00370; LRR; 1.
R SAMRT; SM00370; LRRYT; 1.
R SAMRT; SM00370; LRRYT; 1.
R SAMRT; SM00370; LRRYT; 1.
R Glycoprotein; Extracellular matrix; Proteoglycan; Repeat; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 338;
                                                                                                                                                                                                                            Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
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N-LINKED (GLCNAC.
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CYS-RICH.
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LRR-S 3.
LRR-T 5.
LRR-T 6.
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LRR-T 7.
LRR-T 8.
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LRR-T
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                                                                                                                                                               STRAIN-Sprague-Dawley; TISSUE=Eye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            338 AA; 38279 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (DEC'1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May be implicated in biomineralization processes. Has a function in binding of osteoblasts via the alpha(V)beta(3)-
91 DLQWLILDHNLLENSKIKGKVFSKLKQLKKLHINYNNLTESVGPLPKSLQDLQLANNKIS 150
                                                  KIOKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGLPPTL 242
                                                                                                           151 KL--GSFDGLVNLTFIYLQHNQLKEEAVS-ASLKGLKSLEYLDLSFNQMSKLPAGLPTSL 207
                                                                                                                                                                 LELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDI-ENGSLANIPRVREIHLENNKLK 301
                                                                                                                                                                                                208 LTLYLDNNKITNIPDEYFNRFTGLQYLRLSHNELADSGVPGNSFNISSLLELDLSYNKLK 267
                                                                                                                                                                                                                                                                                                                          268 SIPTVNENLENYYLEV----NKLEKFDVKSFCKILGPLSYSKIKHLRLDGNPLTQSSLP 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohno I., Hashimoto J., Takaoka K., Ochi T., Okubo K., Matsubara K.;
"The cloning of a CDNA for novel genes expressed in human
                                                                                                                                                                                                                                                                          KIPSGLPELK - - YLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        integrin (By similarity). SUBUNIT: Binds the alpha(V)beta(3)-integrin (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- PTM: Sulfated on tyrosine residue(s) (By similarity).
-:- SIMILARITY: BELOWGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SLRPS) FAMILY. CLASS II SUBFAMILY.
-:- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Human osteomodulin gene: intron-exon junctions and chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last amontation update)
05steomodulin precursor (Osteoadherin) (OSAD) (Keratan sulfate
proteoglycan osteomodulin) (KSPG osteomodulin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Extracellular matrix (Potential).
-!- TISSUE SPECIFICITY: Bone-specific.
-!- PTM: Binds keratan sulfate chains (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohno I., Matsubara K., Okubo K.;
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Interpro; IPR001611; LRR.
Interpro; IPR003592; LRR_out.
Interpro; IPR003591; LRR_cyp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew: HGNC:8134; OMD.
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                                                                                                                                                                                                                                                                                                                                                                                  PATFRCV 366
                                                                                                                                                                                                                                                                                                                                                                                                                                        323 PDMYECL 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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DD7C0
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Leucine-rich repeat transmembrane protein FLRT1 precursor
(Fibronectin-like domain-containing leucine-rich transmembrane protein 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 -NIPMHIQQLYLQFNEIEAVTANSFINATHLKEINLSHNKIKSQKIDYGVFAKLPNLLQL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 HLEHNNLEEFPFPLPKSLERLLGYNEISKLQTNAMDGLVNLTMLDLCYNYLHDSLLKDK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 AFEGV-TVFHIRIAEAKLISVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGN 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 IFAKMEKLMQLNLCSNRLESMPPGLPSSLMYLSLENNSISSIPEKYFDKLPKLHTLRMSH 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NKITDIENGSLANIPRVREIHLENNKLKK---IPSGLPELKYLQIIFLHSNSIARVGVND 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 NKLQDIPY-NIFNLPNIVELSVGHNKLKQAFYIPRNLEHL-----YLQNNEIEKMNLTV 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 YLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 TNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKL--TKIHPKAFLTTKKLRRL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 DDDDDDDDDDDDDDDDSLFPTREPRSHFFPFDLFPM-CPFGCQC---YSRVVHCSDLGLTSVP 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 DEDYDQEPDDDYQTGFPFRQNVDYGVPFHQYTLGCVSECFCPTNFPSSMYCDNRKLKTIP 87
                                                                                          Extracellular matrix; Proteoglycan;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 421;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CED47B2BC33BB872 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    ASP/GLU-RICH (ACIDIC).
BY SIMLLARITY.
SULFATION (POTENTIAL).
SULFATION (POTENTIAL).
SULFATION (POTENTIAL).
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2.5e-18;
                                                                                                        Signal; Sulfation. POTENTIAL.
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                                                                                                                                           OSTEOMODULIN.
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LRR-T 1.
LRR-T 2.
LRR-T 3.
LRR-T 3.
LRR-T 4.
LRR-T 5.
LRR-T 5.
LRR-T 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320 MCPSIDPLHYHHLTYIRVDONKLK 343
Pfam; PF00560; LRR; 7.
Pfam; PF01462; LRRNT; 1.
SMART; SM001370; LRR; 1.
SMART; SM0013; LRRNT; 1.
SMART; SM00369; LRR TYP; 1.
Cell adhesion; Glycoprotein; Ex
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                                                                                                            repeat;
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29.3%;
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Best Local Similarity 29.3%
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SIGNAL 1
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316
321 AA;
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Q9NZU1;
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MOD_RES
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FLR1_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN
                                                                                                                        Genomics 62:417-426(1999).
-1- FUNCTION: May have a function in cell adhesion and/or receptor
                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat; Repeat; Glycoprotein; Signal.
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LIJINKED (GLCNAC. ..) (POTENTIAL)

N-LINKED (GLCNAC. ...) (POTENTIAL)

FF2BF5DG3CA13092 CRC64;
                                                                                      Lacy S.E., Bonnemann C.G., Buzney E.A., Kunkel L.M.; "Identification of FLRT1, FLRT2, and FLRT3: a novel family of transmembrane leucine-rich repeat proteins.";
                                                                                                                                             SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND GYLCOSYLATION MEDLINE-20112755; PubMed=10644439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                     EMBL; AF169675; AAF28459.1; ALT_INIT.
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LRR 5.
LRR 6.
LRR 7.
LRR 9.
LRR 9.
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InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71359 MW;
                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003961; FN_III.
InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane, Leucine-rich SIGNAL 1 20 CHAIN 21 646
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01462; LRRNT; 1.
Pfam; PF01463; LRRCT; 1.
PRINTS; PR00019; LEURICHRPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM00082; LRRCT; 1.
SM00013; LRRNT; 1.
SM00369; LRR_TYP; 1
                                                                                                                                                                                                                                                                                                                                  HGNC:3760; FLRT1.
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1121
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Pfam; PF00560; LRR; 7.
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             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               646 AA;
                                            NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBGNIT: Binds the basement membrane heparan sulfate proteoglycan perlecan and triple helical collagens type I and type II.
SUBCELLULAR LOCATION: Extracellular matrix.
DOMAIN: The basic amino-terminal ArgyPro-rich binds heparin and heparan sulfate. Binds collagens type I and type II through its
                                                                                194 NALHVLEMSANPLDNNGIEPGAF-EGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKI 252
                                                                                                                                                                                                                     253 STVELEDFKRYKELQRLGLGNNKITD - · IENGSLANIPRVREIHLENNKLKKIPSGLPEL 310
                                                                                                                                                                                                                                             134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGM 193
                                                                                                                                                                               123 PLLEKLHLDDNSVSTVSIEEDAFADSKQLKLLFLSRNHLSSIPSGLPHTLEELRLDDNRI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bengtsson E., Aspberg A., Heinegaard D., Sommarin Y., Spillmann D.; "The amino-terminal part of PRELP binds to heparin and heparan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The leucine-rich repeat protein PRELP binds perlecan and collagens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last anotation update)
Prolargin precursor (Proline-arginine-rich end leucine-rich repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leucine-rich repeat domain.
--- SIMILARIYY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SLRPS) FAMILY. CLASS II SUBFAMILY.
--- SIMILARIYY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bengtsson E., Moergelin M., Sasaki T., Timpl R., Heinegaard D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           !- FUNCTION: May anchor basement membranes to the underlying
                                                                                                                                                                                                                                                                                                                                            242 AHLOKLYLODNAISHIPYN----TLAKMRE--LERLDLSNN 276
                                                                                                                                                                                                                                                                                                    311 KYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNN 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and may function as a basement membrane anchor"; J. Biol. Chem. 277:15061-15068(2002).
26 CPSVCRCDNGFIYCNDRGLTSIPADIPDDATTLYLQNNQI-
                                                                                                                                                                                                                                                                                                                                                                                                                                               381 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol. Chem. 275:40695-40702(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20576219; PubMed=11007795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF163568; AAG23723.1; -. InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Articular cartilage;
                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     connective tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=11847210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9913;
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ID PRLP_BOVIN
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51; Mismatches 105; Indels 33; Gaps

18.2%; Score 363.5; DB 1; Length 646; 32.7%; Pred. No. 6.4e-18;

Pred. No. 6.4e-18;

92; Conservative

Matches

Best Local Similarity

Query Match

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  104 RMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSE 163
                                                                                                                                                                                                                                                                                                                                                         164 VPAALPRNLEQLRLSQNQISRIPPGVFSKLENLLLLDLQHNKLSDGVFKPDTFQGLKNLM 223
                                                                                                                                                                                                                                                                                                                                                                                                                223 HIRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITD--IE 280
                                                                                                                                                                                                                                                                                                                DDDDEDNSLFPTREPRSHFFPFDLFPMCPFGCQC---YSRVVHCSDLGLTSVPTNIPFDT 103
                                                                                                                                                                                                                                                                                                                               49 DEPTEPTDLPPPLPPG----PPSVFPDCPRECYCPPJFPSALYCDSRNLRKVPV-IPSRI 103
                                                                                                                                                                                                                                                                                                                                                                               164 IPLNLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVF 222
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Prolargin precursor (Proline-arginine-rich end leucine-rich repeat
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                   Glycoprotein; Extracellular matrix; Repeat; Leucine-rich repeat;
Signal.
                                                                                                                                                                                                                                 N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                               281 NGSLANIPRVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCP 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                          284 KNSF-NISNLLVLHLSHNRISSVPAISSRLEHL---YLNNNSIEKINGTQICP 332
                                                                                                                                                                                                                                                                                 DB 1; Length 381;
                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                23DA99C01BB772A0 CRC64;
                                                                                                                                                                                                                                                                                       ; Pred. No. 4.6e-18; 59; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        382 AA.
                                                                                                                                                                                                                         SIMILARITY
                                                                                                                                                                                                                                                                                18.1%; Score 361.5;
                                                                                          POTENTIAL.
                                                                                                                LKR-S 1.
LRR-T 1.
LRR-T 2.
LRR-T 3.
LRR-T 3.
LRR-T 4.
LRR-T 5.
LRR-T 6.
LRR-T 6.
LRR-T 7.
LRR-T 7.
LRR-T 7.
                                                                                                          CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                        BY
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
Pfam; PF00560; LRR; 10.
Pfam; PF01462; LRRNT; 1.
                                                                                                                                                                                                                                                                 43682 MW;
                                       PRINTS; PRO0019; LEURICHRPT.
SMART; SM00370; LRR; 7.
SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_TYP; 7.
                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                 302
322
361
361
381
201
201
23
                                                                                                                                                                                                                                                                 381 AA;
                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                              87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRLP_HUMAN
P51888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein).
                                                                                                                                                                                                                 DOMAIN
DISULFID
                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                CARBOHYD
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                                                                                                                                                                                                                                                                SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                    -i- FUNCTION: May anchor basement membranes to the underlying connective tissue (By similarity).
-i- SUBUNIT: Binds the basement membrane heparan sulfate proteoglycan perlecan and triple helical collagens type I and type II (By
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-96029633; PubMed-7592739;
Bengtsson E., Neame P.J., Heinegaard D., Sommarin Y.;
"The primary structure of a basic leucine-rich repeat protein, PRELP,
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-97127584; Pubmed-8954791;
Grover J., Chen X.-N., Korenberg J.R., Recklies A.D., Roughley P.J.;
"The gene organization, chromosome location, and expression of a
"S-kpa matrix protein (FRELP) of human articular cartilage.";
Genomics 38:109-117(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity).

SUBGELLUIAR LOCATION: Extracellular matrix (By similarity).

TISSUB SPECIFICITY: Connective tissue.

I DOMAIN: The basic amino-terminal Arg/Pro-rich binds heparin heparan sulfate. Binds collagens type I and type II through leucine-rich repeat domain (By similarity).

SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SIRPS) FAMILY.

SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00013; LRRINT; 1.
SMART; SM00369; LRR_TYP; 1.
Glycoprotein; Extracellular matrix; Repeat; Leucine-rich repeat;
signal; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL).
N -> H (IN DBSNP:9439).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=VAR_011976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-LEU.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROLARGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYS-RICH.
                                                                                                                                    found in connective tissues.";
J. Biol. Chem. 270:25639-25644(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRR-S
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LRR-S
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LRR-T
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LRR-T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U41344; AAC18782.1; -.
U41343; AAC18782.1; JOINED.
; HGNC:9357; PRELP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew; HGNC:9357; PRELP.
MIN; 601914; ...
InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR0003591; LRR_typ.
Pfam; PF00560; LRR.
Pfam; PF01462; LRRNT; 1.
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SEQUENCE FROM N.A
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                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. Biol. Chem. 275:40695-40702(2000).
-!- FUNCTION: May anchor basement membranes to the underlying connective tissue (By similarity).
-!- SUBUNIT: Binds the basement membrane heparan sulfate proteoglycan perlecan and triple helical collagens type I and type II (By
                                                                                 47 DDDDEDNSLFPTREPRSHFFPFDLFPMCPFGCQC---YSRVVHCSDLGLTSVPTNIPFDT 103
                                                                                                                                                                                                                                                              223 HIRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGGGNNKITD--IE 280
                                                                                                            50 DEPAEPTDLPPPLPPG----PPSIFPDCPRECYCPPDFPSALYCDSRNLRKVPV-IPPRI 104
                                                                                                                                            104 RMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSE 163
                                                                                                                                                              164 IPLNLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVF 222
                                                                                                                                                                                                                                  165 VPSALPRNLEQLRLSQNHISRIPPGVFSKLENLLLLDLQHNRLSDGVFKPDTFHGLKNLM 224
                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).

-!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
-!- DOMAIN: The basic amino-terminal Arg/Pro-rich binds heparin and heparan sulfate. Binds collagens type I and type II through its leucine-rich repeat domain (By similarity).
-!- SIMILARITY: BELONGS TO THE SWALL LEUCINE-RICH PROTEOGLYCANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bengtsson E., Aspberg A., Heinegaard D., Sommarin Y., Spillmann D., "The amino-terminal part of PRELP binds to heparin and heparan
                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Prolargin precursor (Proline-arginine-rich end leucine-rich repeat
                                                          15;
                                                                                                                                                                                                                                                                                                                      281 NGSLANIPRVREIHLENNKIKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCP 333
                                                                                                                                                                                                                                                                                                                                        285 KNSF-NISNLLVLHLSHNRISSVPAINNRLEHL---YLNNNSIEKINGTQICP 333
                               DB 1; Length 382;
                            18.0%; Score 358.5; DB 1; Length 30.7%; Pred. No. 7.4e-18; tive 55; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SLRPS) FAMILY. CLASS II SUBFAMILY.
-!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
382 AA; 43809 MW; AlC4E166B7515695 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                           377 AA
                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Connective tissue;
MEDLINE=20576219; PubMed=11007795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Nterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF163569; AAG23724.1; -.
                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                         90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein).
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sulfate."
                                                                                                                                                                                                                                                                                                                                                                                                                           PRLP_RAT
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                                                         Matches
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61 PPSVFPDCPRECYCPPDFPSALYCDSRNLRKVPI-IPPRIHYLYLQNNFITELPVESFKN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 LTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 KIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGLPPTL 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 LELHIDYNKISTVELEDFKRYKELQRLGIGNNKITD--IENGSLANIPRVREIHLENNKL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 HQLYLDSNKIETIPSGYFKDFPNLAFIRMNYNKLSDRGLPKNSF-NISNLLVLHLSHNKI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 PFDLFPMCPFGCQC ---YSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Keratocan precursor (KTN) (Keratan sulfate proteoglycan keratocan).
KERA OR KTCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
                                                                                                                     matrix; Repeat; Leucine-rich repeat;
                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58; Mismatches 121; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                               -LINKED (GLCNAC. . .) (PO
79CBE62534753C46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         le-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              351 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 KKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPT 334
                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.9%; Score 356.5; 30.7%; Pred. No. le-
                                                                                                                                               POTENTIAL.
PROLARGIN.
CYS-RICH.
                                                                                                                                                                                                                                                                                                           LRR-T 6.
LRR-S 4.
LRR-T 7.
LRR-T 8.
POLY-LEU.
BY SIMILA.
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LRR-S
LRR-S
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LRR-S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              43179 MW;
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
                           Pfam; PF00560; LRR; 8.
Pfam; PF01462; LRRNT; 1.
PRINTS; PR00019; LEURICHRPT.
                                                                                                                  Glycoprotein; Extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84; Conservative
                                                                    SMART; SM00370; LRR; 5.
SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_TYP;
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318
357
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315
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84
84
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133
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178
202
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228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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377 AA;
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688
681
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1158
220
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2244
260
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284
315
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035367;
                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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REPEAT
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                                                                                                                                   Signal
                                                                                                                                                                CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                  STRAIN=129/SvJ; TISSUE=Cornea;
MEDLINE=98380483; PubMed=9712886;
Liu C.-Y., Shiraishi A., Kao C.W.-C., Converse R.L., Funderburgh J.L.,
STRAIN-ARR/J X CS7L/J; TISSUE-Eye;
MEDLINE-98191735; PubMed-9530631;
Dunlevy J.R., Chakravarti S., Gyalzen P., Vergnes J.-P., Hassell J.R.;
"Cloning and chromosomal localization of mouse keratocan, a corneal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercations and the statement is not removed.
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N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
B0632B387864B98D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: Binds keratan sulfate chains.
SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SIRPS) FAMILY: CLASS II SUBFAMILY: SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
Leucine-rich repeat; Signal; Sulfation.
SIGNAL 1 20 POTENTIAL.
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LRR-T 8.
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LRR-7
LRR-7
LRR-7
LRR-7
LRR-7
LRR-5
LRR-7
                                                                          keratan sulfate proteoglycan.";
Mamm. Genome 9:316-319(1998).
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Interpro; IPR0015592; LRR_out.
Pfam; PF00560; LRR; 8.
Pfam; PF01462; LRRY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF022256; AAC15505.1; -. EMBL; AF057301; AAC61257.1; -.
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InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00370; LRR; 3.
SMART; SM00013; LRRNT; 1.
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299
351 AA;
                                                                                                                                SEQUENCE FROM N.A.
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01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Fibromodulin precursor (FM) (Collagen-binding 59 kDa protein) (Keratan sulfate proteoglycan fibromodulin) (KSPG fibromodulin).
                                                                                                                                                                                                                                                                                                                                                                                                                                      265 ELQRLGLGNNKITD-----IENGSLANIPRV----REIHLENNKLKKI 303
                                                                                                                                                                                                                                                                 88 SDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKLTK--IHPKAF 145
                                                                                                                                                                                                                                                                                                                                                                                                146 LTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANP 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 LDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 KVAFLRENHNKLSDAGLPSRGFDVSSILDLQLSYNQLTNFPRINANLQHLHLDHNKIKNV 298
                                                                 Gaps
                                                                                                                                  31 LKDMEDTDDDDDDDDDDDDDDDDDDDDDDDSLFPTREPRSHFFPFDLFPMCPFGCQC---YSRVVHC 87
                                                                                                                                                                                                ------FY----FY-----59RECFCPPSFPTALYC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91056119; PubMed=2243109;
Plaas A.H.K., Neame P.J., Nivens C.M., Reiss L.;
"Identification of the keratan sulfate attachment sites on bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE-90060020; PubMed-2531085; Oldberg A., Antonsson P., Lindblom K., Heinegaard D.; "A collagen-binding 59-kd protein (fibromodulin) is structurally related to the small interstitial proteoglycans PG-S1 and PG-S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fibromodulin isolated from articular cartilage.";

Eur. J. Blochem. 242:402-409(1996).

-- FUNCTION: Affects the rate of fibrils formation. May have a primary role in collagen fibrillogenesis (By similarity).

-- SUBGNIT: Binds to type I and type II collagen.

-- SUBGELLULAR LOCATION: Extracellular matrix.

-- PTM: Binds keratan sulfate chains.

-- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
                                                                 62;
Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lauder R.M., Huckerby T.N., Nieduszynski I.A.; "The structure of the keratan sulphate chains attached to
                                                                 60; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 90-105 AND 274-281.
17.3%; Score 345; DB 1; 28.1%; Pred. No. 5.7e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 NMSVICPTTLRAEQDAFIHGPQLSYLRLDGNEIKPPIP 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304 PSGL---PELKYLQIIFLHSNSIA--RVGVNDFCPTVP 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             375 AA.
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Biol. Chem. 265:20634-20640(1990).
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                              28.1%;
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   Query Match 17.39
Best Local Similarity 28.19
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
                                                                                                                                                                                                   29 IQDPEDWDVHDD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9913;
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P13605;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC. . . ) (KERATAN SULFATE).
(GLCNAC. . ) (KERATAN SULFATE).
(GLCNAC. . ) (KERATAN SULFATE).
(GLCNAC. . ) (KERATAN SULFATE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---NIPRVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 YGSPPQPEPRD------CPQECDCPPNFPTAMYCDNRNLKYLPF-VPSRMKYVFFQ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 NNQISSIQEGVFDNATGLLWIALHGNQITSDKVGKKVFSKLRHLERLYLDHNNLTRIPSP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRI 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 LPRSLRELHLDHNQISRVPNNALEGLENLTALYLHHNEIQEVG---SSMKGLRSLILLDL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLA- 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 ----PTREPRSHFFPFDLFPMCPFGCQC---YSRVVHCSDLGLTSVPTNIPFDTRMLDLQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 NNKIKEIKENDFKGLTSLYGLILNNNKLT--KIHPKAFLTTKKLRRLYLSHNQLSEIPLN 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|| ||| : || : || : :| || : :| || 6 ILLLAGLCSLSWAQYEEDSHWWFQ--FLRNQOSTYDDPYDPYPPYEPYPTGEEGPAYA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LLLFLALCSAK--PFFSPSHIALKNMMLKDMEDTDDDDDDD-----DDDDDDDDDDDSLF- 56
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C12317E8252B22B9 CRC64;
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R InterPro; IPR000372; LRR.Nterm.
R InterPro; IPR003591; LRR.Nterm.
R InterPro; IPR003591; LRR.Lyp.
R Pfam; Pr00560; LRR.8; 8.
R Pfam; Pr00462; LRR.7; 1.
SMART; SM00370; LRR.7; 1.
SMART; SM000370; LRR.7; 1.
SMART; SM000370; LRR.7; 1.
SMART; SM00013; LRR.NT; 1.
SMART; SM00013; LRR.TYP; 2.
Glycoprotein; Extracellular matrix; Proteoglycan; Repeat; Jeucine-rich repeat; Signal.
SIGNAL.

SIGNAL.

1 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 375;
(SLRPS) FAMILY. CLASS II SUBFAMILY.
-!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 342.5; DB 1;
Pred. No. 9.2e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
N-LINKED (GLCNAC.
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N-LINKED
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LRR-S 2.
LRR-T 3.
LRR-T 4.
LRR-S 3.
LRR-T 5.
LRR-T 6.
LRR-T 7.
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LRR-T 1
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27.7%;
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    connective tissue (By similarity).
-!- SUBUNIT: Binds the basement membrane heparan sulfate proteoglycan perlecan and triple helical collagens type I and type II (By
287 NTFNSSSLLELDLSYNQLQKIP---PVSTNLENLYLQGNRINEFSISSFCTVVDVMNFSK 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i-TISSUE SPECIFICITY: Expressed in cartilage throughout both fetal development and post-natal life. It is also expressed in the developing embryo prior to skeletogenesis. In adult, highest expression in lung, lower levels in cardiac and skeletal muscle.-i-DOMAIN: The basic amino-terminal Arg/Pro-rich binds heparin and heparan sulfate. Binds collagens type I and type II through its leucine-rich repeat domain (By similarity).
-i-SIMILARIY: CLASS II SUBFAMILY.
-i-SIMILARIY: CLASS II SUBFAMILY.
                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last amoncation update)
Prolargin precursor (Proline-arginine-rich end leucine-rich repeat
                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Extracellular matrix; Repeat; Leucine-rich repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: May anchor basement membranes to the underlying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grover J., Roughley P.J.;
"Characterization and expression of murine PRELP.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Extracellular matrix.
                                                                                                                                                                  378 AA
                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF261888; AAF72994.2; -.
EMBL; AF261887; AAF72994.2; JOINED.
EMBL; BC019775; AAH19775.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Nterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matrix Biol. 20:555-564(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00560; LRR; 8.
Pfam; PF01462; LRRNT; 1.
PRINTS; PR00019; LEGRICHRPT.
SMART; SM00370; LRR; 6.
SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_TYP; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
                                                                                                                                                                  STANDARD;
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                                  343 YSAISLFNNPVK 354
                                                                       344 LQVQRLDGNEIK 355
                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=11731272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity)
                                                                                                                                                                  PRLP_MOUSE
                                                                                                                                                                                                                                                                             protein).
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                                                                                                                                                                                                                                                                                                                                           67 PFDLFPMCPFGCQC---YSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKG 123
                                                                                                                                                                                                                                                                                                                                                          124 LTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVK 183
                                                                                                                                                                                                                                                                                                                                                                                                           184 KIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGLPPTL 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 RIPPGVFSKLENLLLLDLQHNRLSDGVFKADTFQGLKNLMQLNLAHNILRKMPPKVPQAI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 LELHLDYNKISTVELEDFKRYKELQRLGLGNNKITD--IENGSLANIPRVREIHLENNKL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 HQLYLDSNKIETIPNGYFKDFPNLAFIRMYNKLSDRGLPKNSF-NISNLLVLHLSHNKI 299
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KERA_BOVIN STANDARD; PRT; 352 AA.
062702; 028032;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Keratocan precursor (KTN) (Keratan sulfate proteoglycan keratocan)
(KSPG keratocan) (Corneal keratan sulfate proteoglycan 37A core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                    . .) (POTENTIAL)
                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                  58; Mismatches 122; Indels 11;
                                                                                                                                                                                                                                                                                           17.2%; Score 342.5; DB 1; Length 378;
                                                                                                                                                                                                                                                                  81654FB9D5F55186 CRC64;
                                                                                                                                                                                                                                                                                                        Pred. No. 9.3e-17;
                                                                                                                                                                                                                N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                      GLCNAC
                                                                                                                                                                                                    BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 KKIPSGLPELKYLQIIFLHSNSIARVGVNDFCP 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 SNVPAISNKLEHL --- YLNNNSIEKINGTQICP 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND TISSUE SPECIFICITY
             PROLARGIN
                         CYS-RICH.
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MEDLINE-98426158; PubMed-9751803;
                                                                                                                                                                                                                                                              43292 MW;
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                                                                                                                                                                                                                                                                                                                  82; Conservative
                                                                                                                                                                         378
198
369
120
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316
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                                                                                                                                                                                                                                                    323
378 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. ..) (FOTENTIAL).
(BY SIMILARITY).
N-LINKED (GLCNAC. ..) (FOTENTAN SULFATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
(BY SIMILARITY).
                                                                                                                                                                                                                                         . .) (KERATAN SULFATE)
                                                                                                                                                                      J. Biol. Chem. 266:14226-14231(1991).
-!- FUNCTION: May be important in developing and maintaining corneal transparency and for the structure of the stromal matrix (By
                                                                                                                                                                                                                   -!- SUBCELLULÁR LOCATION: Extracellular matrix (Potential).
-!- TISSUE SPECIFICITY: Abundant in cornea and sclera but also found
                                Corpuz L.M., Funderburgh J.L., Funderburgh M.L., Bottomley G.S.,
                                           Prakash S., Conrad G.W.;
Molecular cloning and tissue distribution of keratocan. Bovine "orneal keratan sulfate proteoglycan 37A.";
J. Biol. Chem. 271:9759-9763(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U48360; AAC48568.1; -.

R InterPro; IPR001611; LRR.
InterPro; IPR001612; LRR_uterm.
InterPro; IPR00352; LRR_out.
Pfam; PF00560; LRR; 7.
R Fam; PF00560; LRR; 7.
SMART; SM00013; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
V Glycoprotein; Extracellular matrix; Proteoglycan; Repeat; Leucine-rich repeat, Signal; Sulfation.
CHAIN

21 352 KERATOCAN.
                                                                                                                                      Funderburgh J.L., Funderburgh M.L., Mann M.M., Conrad G.W., "Unique glycosylation of three keratan sulfate proteoglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY)
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LRR-T 1.
LRR-T 3.
LRR-T 3.
LRR-T 3.
LRR-T 4.
LRR-T 5.
LRR-T 5.
LRR-T 6.
LRR-T 6.
LRR-T 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYS-RICH.
                                                                                                    PARTIAL SEQUENCE, AND CARBOHYDRATES.
                                                                                                                           MEDLINE=91317768; PubMed=1907274;
          TISSUE=Cornea;
MEDLINE=96199241; PubMed=8621655;
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF036962; AAC69272.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222
260
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SEQUENCE FROM N.A.
                                                                                                                                                                                                            similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222
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                                                                                                                TISSUE-Cornea;
                                                                                                                                                             isoforms."
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                                                                                                                                           131 ILNNNKLTK - - IHPKAFLTTKKLRRLYLSHNOLSEIPLNLPKSLAELRIHENKVKKIQKD 188
                                                                                                                                                                                                                     101 NLNKNKITNYGIEKGALSQLKKLLFLFLEDNELEEVPSPLPRSLEQLQLARNKVSRIPQG 160
                                                                                                                                                                                                                                                                                                                            DYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLA-NIPRVREIHLENNKLKKIPSG 306
                                                                                                                                                                                                                                                                                         161 TFSNLENLTLLDLOHNKLLDNAFORDTFRGLKNLMQLNMAKNALRNMPPRLPANTMQVFL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invest. Ophthalmol. Vis. Sci. 42:3118-3122(2001).
-!- FUNCTION: May be important in developing and maintaining corneal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Regatocan precursor (KTN) (Keratan sulfate proteoglycan keratocan).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pellegata N.S., Dieguez-Lucena J.L., Joensuu T., Lau S.,
Montgomery K.T., Krahe R., Kivelae T., Kucherlapati R., Forsius H.,
de la Chapelle A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21583600; PubMed-11726611;
Lebhann O.J., El-ashry M.F., Ebenezer N.D., Ocaka L., Francis P.J.,
Wilkie S.E., Patel R.J., Ficker L., Jordan T., Khaw P.T.,
Bhattacharya S.S.;
                                                                                                                                                                                                                                                       189 TFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGLPPTLLELHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structure and sequence of the gene encoding human keratocan."; DNA Seq. 10:67-74(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wentz-Hunter K., Cheng E.L., Ueda J., Sugar J., Yue B.Y.J.T., "Keratocan expression is increased in the stroma of keratoconus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A novel keratocan mutation causing autosomal recessive cornea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tasheva E.S., Funderburgh J.L., Funderburgh M.L., Corpuz L.M.,
                                              17.1%; Score 340.5; DB 1; Length 352; 31.9%; Pred. No. 1.2e-16; Live 52; Mismatches 121; Indels 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Mutations in KERA, encoding keratocan, cause cornea plana.";
R -> K (IN REF. 2).
EC708F46AF041A94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE FROM N.A., AND VARIANT CNA2 SER-247.
MEDLINE-20264376; Pubmed=10802664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      352 AA
                                                                                                                                                                                                                                                                                                                                                                                             307 LPELKYLQIIFLHSNSIARVGVNDFCPTVP 336
                                                                                                                                                                                                                                                                                                                                                                                                                    REGULATION IN KERATOCONUS CORNEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                40433 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genet. 25:91-95(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Med. 7:470-477(2001).
                                                                 Local Similarity 31.9:
nes 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens (Human).
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                352 AA;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                               corneas. Reratoconus is a noninflammatory disease characterized by thinning and scarring of the central portion of the cornea. SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SLRPS) FAMILY. CLASS II SUBFAMILY.
SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
transparency and for the structure of the stromal matrix. SUBCELULAR LOCATION: Extracellular matrix (Potential).

IISSUE SPECIFICITY: Cornea. Also detected in trachea, and in low levels, in intestine, skeletal muscle, ovary, lung and putamen. PTM: Binds keratan sulfate chains (By similarity).

DISBASE: Defects in KERA are the cause of the autosomal recessive cornea plana 2 (CNA2). In CNA2, the forward convex curvature is flattened, leading to a decrease in refraction, reduced visual activity, extreme hyperopia (usually plus 10 d or more), hazy corneal limbus, opacities in the corneal parenchyma, and marked arcus senilis (often detected at an early age). CNA2 is a rare disorder with a worldwide distribution, but a high prevalence in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
SULFATION (POTENTIAL).
N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . .) (KERATAN SULFATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00370; LRR; 3.
SMART; SM00013; LRRNT; 1.
SLAPOPTOTATION: Extracellular matrix; Proteoglycan; Repeat;
Leucine-rich repeat; Signal; Sulfation; Disease mutation; Vision.
SIGNAL 1 20 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                       the Finnish population.
DISEASE: Increased expression in the stroma of keratoconus
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0CF8DEC938852D28 CRC64;
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/FTId=VAR_013564.
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N-LINKED (GLCNAC.
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LRR-T 7.
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LRR-T
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InterPro; IPR000372; LRR_Nerm.
InterPro; IPR003592; LRR_out.
Pfam; PF00560; LRR; 8.
Pfam; PF01462; LRRNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF065988; AAC17741.1; -. EMBL; AF063301; AAC16390.1; -. EMBL; AF205403; AAF69126.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HGNC: 6309; KERA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew; HGNC:6309
MIM; 603288; -.
MIM; 217300; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
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40509 MW;

352 AA;

SEQUENCE

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01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Fibromodulin precursor (FM) (Collagen_binding 59 kDa protein) (Keratan
                                                                               74 CPFGCQC---YSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGL 130
                                                                                                                  42 CPMECFCPPSFPTALYCENRGLKEIPA-IPSRIWYLYLQNNLIETIPEKPFENATQLRWI 100
                                                                                                                                                          131 ILNNNKLTK--IHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKD 188
                                                                                                                                                                                   189 TFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGLPPTLLELHL 247
                                                                                                                                                                                                                                                                                                                        DYNKISTVELEDFKRYKELQRLGLGNNKITD-------IENGSLANIPRV 290
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                                                                                                                                                                                                                                                                                                                                                                                                   ----REIHLENNKLKKI------PSGL-----PELKYLQIIFLHSNSIARVGV 328
                                                                                                                                                                                                                                                                                                                                                                                                                                             281 SAHLQHLHLDHNKIKSVNVSVICPSPSMLPAERDSFSYGPHLRYL------RLDG 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                       Gaps
                                                                                                                                                                                                                                                                -!- FUNCTION: Affects the rate of fibrils formation. May have a primary role in collagen fibrillogenesis (By similarity).
-!- SUBGNIT: Binds to type I and type II collagen (By similarity).
-!- SUBCELLULAR LOCATION: Extracellular matrix.
-!- PTM: Binds keratan sulfate chains (By similarity).
-!- SIMILARITY: BELONGS TO THE SMALL LEUCINB-RICH PROTEOGLYCANS (SLRPS) FAMILY. CLASS II SUBFAMILY.
-!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
                                       57;
DB 1; Length 352;
                                     54; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sulfate proteoglycan fibromodulin) (KSPG fibromodulin)
17.1%; Score 340.5; DB 1
29.2%; Pred. No. 1.2e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X82152; CAA57648.1; -.
InterPro; IPR001611; LRR.
InterPro; IPR00372; LRR.Nterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
Pfam; PF00560; LRR; 9.
                                       90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRRNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Sprague-Dawley;
                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  329 NDFCPTVP 336
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Query Match
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57 ---PTREPRSHFFPFDLFPMCPFGCQC---YSRVVHCSDLGLTSVPTNIPFDTRMLDLQN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 NKIKEIKENDFKGLTSLYGLILNNNKLT--KIHPKAFLTTKKLRRLYLSHNQLSEIPLNL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 EAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLA-- 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232 YNHLRRVPDGLPSALEQLYLEHNNVYTVPDSYFRGSPKLLYVRLSHNSLT---NNGLATN 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 --NIPRVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLY 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 TFNSSSLLELDLSYNQLQKIP---PVNTNLENLYLQGNRINEFSISSFCTVVDVMNFSKL 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 GAPPPPEPRD------CPQECDCPPNFPTAMYCDNRNLKYLPF-VPSRMKYVYFQN 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 NQIAAIQEGVFDNATGLLWIALHGNQITSDKIGRKVFSKLRHLERLYLDHNNLTRMPGPL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIA 227
                                                                                                                                                                                                                                                                                         . .) (KERATAN SULFATE)
                                                                                                                                                                                                                                                                                                                   . .) (KERATAN SULFATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                 . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                    17.0%; Score 338; DB 1; Length 376; 28.0%; Pred. No. 1.9e-16;
SMART; SM00370; LRR; 1.
SMART; SM00013; LRRNT; 1.
SMART; SM00013; LRR TYP; 1.
Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
Leucine-rich repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              65; Mismatches 160; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           9C3298675CE3714A CRC64;
                                                                                                                                                                                                                                                                              BY SIMILARITY.
N-LINKED (GLCNAC.
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OMD_BOVIN STANDARD; PRT; 422 AA. 077742; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY)
                                                                     BY SIMILARITY.
                                                                                  FIBROMODULIN.
                                                                                              CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.
                                                                                                        LRR-S 1.
LRR-T 1.
                                                                                                                                 LRR-T 2.
LRR-S 2.
LRR-T 3.
LRR-T 4.
LRR-S 3.
LRR-T 5.
LRR-T 6.
LRR-S 4.
LRR-S 7.
                                                                                                                                                                                                                                                                   POLY-PRO
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                                                                                                                                                                                                                                                                                                                                                                                                341 3
376 AA;
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OMD_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                 J. Cell Biol. 141:839-847(1998).
-1- FUNCTION: May be implicated in biomineralization processes. Has a function in binding of osteoblasts via the alpha(V)beta(3)-
                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBGUNIT: Binds the alpha(V)beta(3)-integrin.
SUBCELULAR LOCATION: Extracellular matrix (Potential).
TISSUE SPECIFICITY: Bone-specific.
PTM: The N-terminus is blocked.
PTM: Some of the oligosaccharides are extended to keratan sulfate
                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 28-35; 119-126; 132-139; 191-198 201-207; 264-268; 294-300 AND 377-381.
                                                                                                                                                                                                                                                                                                                           Wendel M., Sommarin Y., Heinegaard D.; "Bone matrix proteins: isolation and characterization of a novel cell-binding keratan sulfate proteoglycan (osteoadherin) from bovine
                                                                                                                                                                                                            in bone,
                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Extracellular matrix; Proteoglycan; Signal; Sulfation.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: Sulfated on tyrosine residue(s) (Probable).
SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SLRPS) FAMILY. CLASS II SUBFAMILY.
SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
Osteomodulin precursor (Osteoadherin) (OSAD) (Keratan sulfate proteoglycan osteomodulin) (KSPG osteomodulin).
                                                                                                                                                                                       Sommarin Y., Wendel M., Shen Z., Hellman U., Heinegaard D., "Osteoadherin, a cell binding keratan sulfate proteoglycan ir belongs to the family of leucine-rich repeat proteins of the extracellular matrix.":
                                                                                                                                                                                                                                                                              SEQUENCE OF 119-126 AND 191-198, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OSTEOMODULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
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LRR-T 1.
LRR-S 2.
LRR-S 2.
LRR-T 3.
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LRR-S
LRR-T
LRR-T
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LRR-T
LRR-T
LRR-T
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InterPro; IPROOLG11; LRR.
InterPro; IPROOLG32; LRR.Nterm.
InterPro; IPROOLG352; LRR.nterm.
InterPro; IPROOLG52; LRR.nt.
IPfam; PFOOLG62; LRRN; 1.
SMART; SMOORG3; LRRN; 2.
SMART; SMOOG013; LRRN; 1.
Cell adhesion; Glycoprotein; Extri
Repeat; Leucine-rich repeat; Signi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U67279; AAC39259.1; -.
                                                                                 Bovidae; Bovinae; Bos. NCBI_TaxID=9913;
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422
78
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103
127
1153
1153
                                                                                                                                                                                                                                   extracellular matrix.
                                            taurus (Bovine).
                                                                                                                                                            TISSUE=Osteoblast;
                                                                                                                                                                                                                                                                                             TISSUE=Bone;
PubMed=9566981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21
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207 VLAKMEKLMQLNLCNNRLESMPPGLPSSLMYLSLENNSISSIPENYFNKLPKLHALRISH 266
                                                                                                                                                                                                                                                                                                                             215 AFEGV-TVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGN 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 NKITDIENGSLANIPRVREIHLENNKLKK---IPSGLPELKYLQIIFLHSNSIARVGVND 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 NKLQDIPY-NIFNLSNLIELNVGHNKLKQAFYIPRNLEHL-----YLENNEIENVNVTV 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                  155 YLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPG 214
                                                                                                                                                                                                                                                                             DDDDDDDDDDDDDDDDDDDTFPTREPRSHFFPFDLFPM-CPFGCQC---YSRVVHCSDLGLTSVP 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nurminskaya M.V., Birk D.E.; "Differential expression of fibromodulin mRNA associated with tendon fibril growth: isolation and characterization of a chicken
                                                                                                                                                                                                                                                                                              28 DEDYDQEPDDVYQTEFQFQQNINYEAPFHQHTLGCASECFCPPNFPSSMYCDNRKLKTIP
                                                                                       N-LINKED (GLCNAC...) (POTENTIAL).
L -> R (IN REF. 2).
C -> Y (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    primary role in collagen fibrillogenesis (By similarity). SUBUNIT: Binds to type I and type II collagen (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. J. 317:785-789(1996).
-!- FUNCTION: Affects the rate of fibrils formation. May have a
                                                                                                                                                                                                                          Length 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fibromodulin precursor (FM) (Keratan sulfate proteoglycan fibromodulin) (KSPG fibromodulin).
                                                                                                                                                                                                                                                 75; Mismatches 141; Indels
                                                                                                                                                                                                3C349C3D6B59F5AD CRC64;
                                                 SULFATION (POTENTIAL).
SULFATION (POTENTIAL).
SULFATION (POTENTIAL).
                          ASP/GLU-RICH (ACIDIC).
BY SIMILARITY.
                                                                                                                                                                                                                          17.0%; Score 338; DB 1; 27.8%; Pred. No. 2.2e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331 FCPTVPKMKKSLYSAISLFNNPVK 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fibromodulin cDNA.";
Biochem. J. 317:785-789(1996).
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 342
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t Local Similarity
ches 90; Conserv
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313 PRVSTNLENL---YLQGNQINEFSISSFCTVVDVMNYSRLQVLRLDGNEIKRNAMPPDAP 369

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                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the between the Swiss Institute of Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 CPFGCQC---YSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 CPQECDCPPNFSSAMYCDTRNLRYLPF-VPTRMKYVYFQNNQITAIQEGAFDNATELEWL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 ILNNNKLT--KIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKD 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 ALHNNQISSEKMGKRVFAKLKNLERLYMNNNLTKMPSPLPRSLRELHLSYNQISKVPSN 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EYNYINAIPDDYFKVSPKLLYVRMSHNSLT---NQGLSTNTFNSSSILELDLSYNRLQKI 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . .) (KERATAN SULFATE)
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               PTM: Binds keratan sulfate chains (By similarity). SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Pred. No. 3.9e-16;
61; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                    Pfam; PF00560; LRR; 9.
Pfam; PF01462; LRRWT; 1.
SMART: SW00013; LRRWT; 1.
Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <del>..</del>
                                                     (SLRPS) FAMILY. CLASS II SUBFAMILY.
SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F4613B3CA7FF0E4D CRC64;
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SUBCELLULAR LOCATION: Extracellular matrix
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InterPro; IPR000372; LRR_Nterm.
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MEDLIND-21638749; PubMed=11780052;

MEDLIND-21638749; PubMed=11780052;

A Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

A Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,

Bassley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Buck D., Burtill W.D., Buller A.P., Carder C., Carter N.P.,

Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,

RA Coulson A., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

Coulson A., Coville G.J., Deadman R. Dhami P.D., Dunn M.,

Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Hammond S., Harley J.L., Heath P.D., HO S., Holden J.L., Howden P.J.,

RA Hammond S., Harley J.L., Heath P.D., HO S., Holden J.L., Howden P.J.,

RA Hammond S., Harley J.L., Heath P.D., HO S., Holden J.L., Rowell J.D.,

RA Ray M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,

Allorer K., Parker A., Patel R., Pearce T.A.V., Peck A.L.,

RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,

RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,

RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,

Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDILINE-20277482; PubMed=10819331;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
Nprediction of the coding sequences of unidentified human genes. XVII.
The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 7:143-150(2000).
                                                                                                                                                                                                                                                                                                                                             FLR3_HUMAN STANDARD;

Q9NZUO, 096KB1; Q9PSS9; Q96K42; Q96K39;

15-JUN-2002 (Rel. 41, Created)

15-JUN-2002 (Rel. 41, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

16-JUN-2002 (Rel. 41, Last annotation update)

16-Ucine-rich repeat transmembrane protein FLRT3 precursor

(Fibronectin-like domain-containing leucine-rich transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

TISSUE-Embryo, and Teratocarcinoma;

TISSUE-Embryo, and Teratocarcinoma;

TISSUE-Embryo, and Teratocarcinoma;

TISSUE-Embryo, and Teratocarcinoma;

Nishikawa T., Nagal, K., Sugino S., Shiratori A., Sudo H.,

Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

Ninomilya K., Irayanagi T.;

"NEDO human cDNA sequencing project.";

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lacy S.E., Bonnemann C.G., Buzney E.A., Kunkel L.M.; "Identification of FLRT1, FLRT2, and FLRT3: a novel family of transmembrane leucine-rich repeat proteins."; Genomics 62:417-426(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND TISSUE SPECIFICITY. MEDLINE=20112755; PubMed=10644439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
364 RCVLSRMSV 372
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                                                                                        370 LC-LRRATV 377
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                                                                                                                                                                                   -1- TISSUE SPECIFICITY: Expressed in kidney, brain, pancreas, skeletal muscle, lung, liver, placenta, and heart.
-1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
-1- SIMILARITY: CONTAINS 10 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN
Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A. Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.
                                                              "The DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                                        Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: May have a function in cell adhesion and/or receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat; Repeat; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIBRONECTIN TYPE-III.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                            signaling.
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                                                                                                                                                                                                                                                                                                                                              EMBL; AF169677; AAF28461.1; -.
EMBL; AB040902; BAA95993.1; ALT_INIT.
EMBL; AK027297; BAB55023.1; -.
                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AKO27670; BAB55282.1; ALT_INIT.
EMBL; AKO27694; BAB55303.1; ALT_INIT.
EMBL; AL132826; CAB86687.1; -:
EMBL; BC020870; AAH20870.1; -:
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Interpro; IPR000483; LRR.Cterm.
Interpro; IPR000372; LRR.Nerm.
Interpro; IPR003592; LRR.out.
InterPro; IPR003591; LRR.Lyp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_TYP; 1.
Transmembrane; Leucine-rich
                                                                      Nature 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01462; LRRNT; 1.
Pfam; PF01463; LRRCT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    HGNC:3762; FLRT3.
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Pfam; PF00560; LRR; 10.
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SMART; SM00370; LRR; 1.
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SMART;
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primary role in collagen fibrillogenesis.
SUBUNIT: Binds to type I and type II collagen.
SUBCELGUARA LOCATION: Extracellular matrix.
TISSUE SPECIFICITY: Highest levels observed in knee epiphysis, in calvarial and diaphyseal bone, in nasal and costal cartilage, in the eye, and in bladder. In mature knee joint it is mostly present in the proliferating zone of growth plate. It is also observed in ligaments, especially at insertion sites, in the junction between meniscus and joint capsule, in the perimysium of skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein) (Keratan
                                                                                                                                                                                                                                                                                74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
                                                                                                                                                                                                                                                            134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGM 193
                                                                                                                                                                                                                                                                                                                                                                                                    STVELEDFKRYKELQRLGLGNNKITDIENGS--LANIPRVREIHLENNKLKKIPSGLPEL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                    188 STISSPSLQGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPMENTAL STAGE: Highest levels between 5 days and 1 month of age. Thereafter, the expression of declined to a level of approx. 35% of maximum, and remained constant throughout the rest of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seaaemaenen A.-M.K., Salminen H.J., Rantakokko A.J., Heinegaard D.,
                                                                                                                                                                                                                                                                                                                                194 NALHVLEMSANPLDNNGIEPGAFEGVTVFHIR-IAEAKLTSVPKGLPPTLLELHLDYNKI
                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Murine fibromodulin: cDNA and genomic structure, and age-related expression and distribution in the knee joint.";
Biochem. J. 355:577-585(2001).
-i- FUNCTION: Affects the rate of fibrils formation. May have a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                observation period.

PTM: Binds keratan sulfate chains (By similarity).

PTM: Sulfated on tyrosine residue(s) (Probable).

SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
                                                                                                                       16.6%; Score 331.5; DB 1; Length 649;
                                                   BAB55023).
                                     BAB55023)
                                                                                                                                                         37; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Fibromodulin precursor (FM) (Collagen-binding 59 kDa pr
sulfate proteoglycan fibromodulin) (KSPG fibromodulin).
 L -> P (IN REF. 3; B
W -> R (IN REF. 3; B
H -> Q (IN REF. 3; B
D -> G (IN REF. 3; B
D -> G (IN REF. 3; B
D -> G (IN REF. 3; B
                                                                                                                                                                                                            Pred. No. 1e-15,
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198 L
307 W
400 H
519 K
638 D
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                                                                                                                                          33.0%;
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                                                                                                                                                       Conservative
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                                                                                   649 AA;
                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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 198
307
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P50608;
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                                                                                                                                          Best Loc
Matches
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TISSUE=Cornea;
                          347 SLFNNPVK
                                                                                       KERA_CHICK
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REPEAT
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                                                                               KERA_CHICK
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                                           q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 LAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231 LTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLA---N 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 LRRVPDGLPSALEQLYLEHNNVYTVPDSYFRGSPKLLYVRLSHNSLT---NNGLATNTFN 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             287 IPRVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAI 346
                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 KEIKENDFKGLTSLYGLILNNNKLT--KIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKS 171
                                                                                                                                                                                                                                                                                                                                                                                                             . .) (KERATAN SULFATE)
                                                                                                                                                                                                                                                                                                                                                                                                                               . .) (KERATAN SULFATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131; Indels 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 376;
                                                                                        SMART; SM00370; LRR; 1.
SMART; SM00310; LRRUT; 1.
SMART; SM0013; LRR_TYP; 1.
Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
Leucine-rich repeat; Signal; Sulfation.
SIGNAL
1 18
BY SIMILARITY.
CHAIN 19 376 FIBRONDULIN.
        SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        45A9EDDB0BADA85B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 331; DB 1;
; Pred. No. 5.7e-16;
57; Mismatches 131;
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LRR-S 3.
LRR-T 5.
LRR-T 6.
(SLRPS) FAMILY. CLASS II SUBFAMILY
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LRR-T 7.
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LRR-S
LRR-T
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                                                                                                       MGD; MGI:1328364; Fmod.
InterPro; IPR001611; LRR.
InterPro; IPR00372; LRR.Uterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        43054 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.6%;
29.2%;
                                                                                                 EMBL; X94998; CAA64454.1; -.
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                                                                                                                                                   Pfam; PF00560; LRR; 9.
Pfam; PF01462; LRRNT; 1.
                                                                                                                                                                                                                                                               167
188
212
235
235
2280
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3305
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335
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367
127
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141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dunlevy J.R., Neame P.J., Vergnes J.-P., Hassell J.R.; "Identification of the N-linked oligosaccharide sites in chick corneal
292 SSSLLELDLSYNQLQKIP---PWNTNLENLYLQGNRINEFSISSFCTVVDVMNFSKLQVL 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Keratocan precursor (KTN) (Keratan sulfate proteoglycan keratocan).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transparent matrix within the corneal strona.
--- SUBCELLULAR LOCATION: Extracellular matrix.
--- PTM: Binds keratan sulfate chains.
--- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SLRPS) FAMILY. CLASS II SUBFAMILY.
--- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., SEQUENCE OF 74-92; 212-220 AND 250-267, AND CARBOHYDRATE-LINKAGE SITES ASN-94; ASN-223 AND ASN-261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001511; LRR.
InterPro; IPR000372; ILRR.Nterm.
InterPro; IPR003592; LRR_Out.
Pfam; PF015650; LRR; 8.
Pfam; PF01462; LRRNT; 1.
SMART; SM00319; LRRNT; 1.
Glycoprotein; Extracellular matrix; Proteoglycan; Repeat; Leucine-rich repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lumican and keratocan that receive keratan sulfate.";
J. Biol. Chem. 273:9615-9621(1998).
                                                                                                                                                                                                                                                                                                                                          353 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
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LRR-T 1.
LRR-T 2.
LRR-S 2.
LRR-T 3.
LRR-T 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20179630; PubMed=10712821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98211990; PubMed=9545293;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108
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84
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                                                                                                                                                                       349 RLDGNEIK 356
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                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (KERATAN SULFATE).
N-LINKED (GLCNAC. . .) (KERATAN SULFATE).
N-LINKED (GLCNAC. . .) (POTENTIAL).
CBF42601FDF33ED6 CRC64;
                                                                                                              (KERATAN SULFATE).
                                                                                                                                                                                                                                                                                     53 NSLFPTREPRSHFFPFDLFPMCPFGCQC---YSRVVHCSDLGLTSVPTNIPFDTRMLDLQ 109
                                                                                                                                                                                                                                                                                                                                                                    168 LPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRI 226
                                                                                                                                                                                                                                                                                                                                                                                                                                      141 LPVGLEQLRLARNKISRIPEGVFSNLENLTMLDLHQNNLLDSALQSDTFQGLNSLMQLNI 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 AEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITD---IENGS 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 AKNSLKKMPLSIPANTLQLFLDNNSIEVIPENYFSAIPKVTFLRLNYNKLSDDGIPPNG- 259
                                                                                                                                                                                                                                                                                                                                                110 NNKIKEIKENDFKGLTSLYGLILNNNKLTK--IHPKAFLTTKKLRRLYLSHNQLSEIPLN 167
                                                                                                                                                                                                                                       ; Pred. No. 1.4e-15; 50; Mismatches 127; Indels 22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coturnix coturnix japonica (Japanese quail),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                       29 NELDP--EHWSH-YIFE----CPQECFCPPSFPNALYCDNKGLKEIPA-IPARIWYLYLQ 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECUENCE FROM N.A.

SECUENCE FROM N.A.

MEDLINE-20566470; Pubmed-11102758;

Corpuz L.M., Dunlevy J.R., Hassell J.R., Conrad A.H., Conrad G.W.;

Molecular cloning and relative tissue expression of keratocan and minecan in embryonic quall cornea.";

Matrix Biol. 19:693-698(2000).

-:- FUNCTION: Play an important role in generating and maintaining transparent matrix within the corneal stroma (By similarity).
-:- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
-:- TISSUE SPECIFICITY: Cornea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Keratocan precursor (KTN) (Keratan sulfate proteoglycan keratocan).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- TISSUE SPECIFICITY: Cornea.
-!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SLRPS) FAMILY. CLASS II SUBFAMILY.
-!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 -FNVSSILDLQLSHNQLTKIP---PINAHLEHLHLDHNRIKSVNGTQICP 305
                                                                                                                                                                                                                        DB 1; Length 353;
                                                                                                                                                                                                                                   1.4e-15;
                                                                                            BY SIMILARITY.
N-LINKED (GLCNAC.
                                                                                                                           (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        353 AA
                                                                                                                                                                                                                      16.3%; Score 325; 31.4%; Pred. No. 1
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LRR-S
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                                                                                                                                                                                        40265 MW;
                                                                                                                                                                                                                                                      91; Conservative
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2226
2220
2275
2275
2295
3344
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168
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2233
2203
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                            . .) (POTENTIAL).
. .) (KERATAN SULFATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 NELDP--EHWSH-YTFE----CPQECFCPPSFPNALYCDNKGLKEIPA-IPARIWYLYLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .) (POTENTIAL)
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                                                InterPro; IPR001611; LRR.

R InterPro; IPR000372; LRR.Nterm.

R InterPro; IPR000372; LRR.Nterm.

R InterPro; IPR00352; LRR.out.

R InterPro; IPR003592; LRR.typ.

R Pfam; PF00560; LRRNT; 1.

R SMART; SM000170; LRRN; 1.

R SMART; SM0001370; LRRN; 1.

R SMART; SM0001370; LRRN; 1.

R SMART; SM0001370; LRRN; 1.

R Glycoprotein; Extracellular matrix; Proteoglycan; Repeat; SIGNAL.

I 21 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - FINYSSILDLOLSHNOLTKIP---PINAHLEHLHLDHNRIKSVNGTOICP 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 353;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.3%; Score 325; DB 1; Length 35: 31.4%; Pred. No. 1.4e-15; tive 50; Mismatches 127; Indels
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N-LINKED (GLCNAC. .) (KERN CS. M. SIMILARITY).

N-LINKED (GLCNAC. .) (POT. W.) DEE07614FC598F7D CRC64;
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N-LINKED (GLCNAC.
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                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY
                                                                                                                                                                                       KERATOCAN
                                                                                                                                                                                                   CYS-RICH.
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LRR-T 7.
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                                            EMBL; AF128223; AAG48156.1; -.
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Matches 91; Conservative
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223
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15-JUN-2002 (Rel. 41, Last annotation update)
Fibromodulin precursor (FM) (Collagen-binding 59 kDa protein) (Keratan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
(BY SIMILARITY).
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                                                                                                                                Antonsson P., Heinegaard D., Oldberg A.; "Structure and deduced amino acid sequence of the human fibromodulin
                                                                                                                                                                                                     Hildebrand A., Twardzik G., Border W.A., Ruoslahti E.;
Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Affects the rate of fibrils formation. May have a
primary role in collagon fibrillogenesis (By Similarity).
-!- SUBGNIT: Binds to type I and type II collagen (By Similarity).
-!- SUBCELLULAR LOCATION: Extracellular matrix.
                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                              -!- PTM: Binds keratan sulfate chains.
-!- FIMILARIYI'S BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SLRPS) FAMILY. CLASS II SUBFAMILY.
-!- SIMILARIYI'S CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWART; SM00370; LRR; 1.
SMART; SM00013; LRRWT; 1.
SMART; SM00019; LRR TYP; 1.
Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
                        sulfate proteoglycan fibromodulin) (KSPG fibromodulin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
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BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIBROMODULIN.
                                                                                                                                                                     Biochim. Biophys. Acta 1174:204-206(1993).
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                                                                                                        SEQUENCE FROM N.A. MEDLINE-93363641; PubMed-8357838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_out.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003591; LRR_typ.
Pfam; PF00560; LRR; 8.
Pfam; PF01462; LRRNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X72913; CAA51418.1; -. EMBL; X75546; CAA53233.1; -. PIR; S32752; S32752. PIR; S35710; S35710; Genew; HGNC:3774; FMOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leucine-rich repeat; Signal.
SIGNAL 1 18
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InterPro; IPR000372; LRR
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                                              Homo sapiens (Human)
                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 600245;
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156 HLERLYLDHNNLTRMPGPLPRSLRELHLDHNQISRVPNNALEGLENLTALYLQHNEIQEV 215
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                                      N-LINKED (GLCNAC. . .) (KERATAN SULFATE) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 LTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKLT--KIHPKAFLTTK 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 KLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNN 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G---SSMRGLRSLYLLDLSYNHLRKVPDGLPSALEQLYMEHNNVYTVPDSYFRGAPKLLY 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGLGNNKITDIENGSLA----NIPRVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIA 324
N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rothberg J.M., Jacobs J.R., Goodman C.S., Artavanis-Tsakonas S.; "Slit: an extracellular protein necessary for development of midline glia and commissural axon pathways contains both EGF and LRR domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa, Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
                                                                                                                                                                                                                                                                                                                                                                                                         37 TYYDPYDPYPYETYEPYPYGVDEGPAYTYGSPSPPDPRDCPQECDCPPNFPTAMYCDNRN 96
                                                                                                                                                                                                                                                                                                                                                                 ----CPFGCQC---YSRVVHCSDLG 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMISSURAL AXON PATHWAYS. SLIT MAY INTERACT WITH EXTRACELLULAR MATRIX MOLECULES.
                                                                              . .) (POTENTIAL).
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-!- FUNCTION: NECESSARY FOR DEVELOPMENT OF MIDLINE GLIA AND
                                                                                                                                                                                                                                                                                    16.3%; Score 325; DB 1; Length 376;
                                                                                                                                                                                                                                                                                                                           130; Indels
                                                                                                                                                                                                                                            C2A78E0678EC3E72 CRC64;
                                                                          N-LINKED (GLCNÁC...
T -> A (IN REF. 2).
P -> L (IN REF. 2).
Y -> I (IN REF. 2).
Y -> I (IN REF. 2).
Q -> K (IN REF. 2).
A -> I (IN REF. 2).
C -> I (IN REF. 2).
E -> D (IN REF. 2).
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01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRI; 1480 AA.
                     (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                           65; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 EFSISSFCTVVDVVNFSQLQVVRLDGNEMK 356
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                                                                                                                                                                                                                                                                                                                                                                     63 SHFFPFDLFPM-------
                                                                                                                                                                                                                                            43246 MW;
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                                                                                                                  87
210
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376 AA;
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201
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                                                                                                                                                                                                                                                                                                                         87;
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CARBOHYD
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                                        CARBOHYD
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FT REPEAT 813 816 LBR 23. FT REPEAT 813 816 LBR 24. FT REPEAT 813 816 LBR 24. FT DOMAIN 907 944 GEF-LIKE 2. FT DOMAIN 907 945 949 GEF-LIKE 2. FT DOMAIN 908 1022 GEF-LIKE 3. CALCIUM-BINDING (POTENTIAL). FT DOMAIN 1064 1100 GEF-LIKE 5. CALCIUM-BINDING (POTENTIAL). FT DOMAIN 1152 1122 GEF-LIKE 5. CALCIUM-BINDING (POTENTIAL). FT DOMAIN 1152 1125 GEF-LIKE 6. FT DOMAIN 1152 1125 GEF-LIKE 6. FT DOMAIN 1152 1125 GEF-LIKE 6. FT CARBOHYD 120 1120 GEF-LIKE 7. FT CARBOHYD 207 377 377 377 1121 1140 FF-LIKED (GLUMC) (POTENTIAL). FT CARBOHYD 207 377 377 FT-LIKED (GLUMC) (POTENTIAL). FT CARBOHYD 207 377 377 FT-LIKED (GLUMC) (POTENTIAL). FT CARBOHYD 120 1159 1159 1159 FT-LIKED (GLUMC) (POTENTIAL). FT CARBOHYD 120 120 120 120 120 120 120 120 120 120	Ouery Match Best Local Similarity 25.1%; Pred. No. 3.4e-14; Matches 98; Conservative 66; Mismatches 123; Indels 104; Gaps Oy 74 CPFGCQCYSRVVHCSDLGLTSVPTNIPEDT
MILARITY: CONTAINS 24 LEUCI MILARITY: CONTAINS 1 C-TERM MILARITY: CONTAINS 1 LAMINI MISS-PROT entry is copyrigh on the Swiss Institute of E ropean Bioinformatics Institutions ed and this statement is no es requires a license agree d and this statement is no es requires a license agree d an email to license(sib.s. 36665; A3666. MISS 1 EDM. PRO0740; LEDM. PRO0740; LEDM. PRO0740; LEDM. PRO00152; Asx.hydroxyl ro; IPR000152; Asx.hydroxyl ro; IPR000561; EGF-1ike. ro; IPR000551; EGF-21. ro; IPR000551; EGF-21. ro; IPR000551; LRR_Out. ro; IPR000551; LRR_Out. ro; IPR000551; LRR_Out. ro; IPR000561; EGF-1ike. ro; IPR00068; EGF-21. ro; IPR00068; EGF-21. SW00069; EGF-21. SW00061; EGF-21. SW00062; LRRY; 4. SW00062; LRRY; 4. SW0062; LRRY; 4. SW0626; L	148 195 195 220 321 345 344 345 344 344 344 344 410 417 417 546 559 510 618 641 720 720 745 745 764

us-09-944-457-2.rsp

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                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Leucine-rich repeat transmembrane protein FLRT2 precursor
(Fibronectin-like domain-containing leucine-rich transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ishikawa K.-I., Nagase T., Nakajima D., Seki N., Ohira M.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. VIII."
78 new cDNA clones from brain which code for large proteins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- TISSUE SPECIFICITY: Expressed in pancreas, skeletal muscle, brain,
227 AEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGGNNKITDIENGSLAN 286
                               309 REKSLTSVPVTLPDDTTDVRLEQNFITELPPKSFSSFRRLRRIDLSNNNISRIAHDALSG 368
                                                                                                            369 LKQLTTLVLYGNKIKDLPSGVFKGLGSLRLLLLNANEISCIRKDAF------RDLHSL 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Res. 4:307-313(1997).
                                                                       IPRVREIHLENNKLKKIPSGL-PELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND GYLCOSYLATION. MEDLINE-20112755; PubMed-10644439;
Lacy S.E., Bonnemann C.G., Buzney E.A., Kunkel L.M.;
"Identification of FLRT1, FLRT2, and FLRT3: a novel family of transmembrane leucine-rich repeat proteins.";
Genomics 62:417-426(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Type I membrane protein (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- SIMILARITY: CÔNTAINS I FIBRONECTIN TYPE III-LIKE DOMAIN.
-:- SIMILARITY: CONTAINS 10 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                    660 AA.
                                                                                                                                                    SAISLFNNPVKYWEMQPATFRCVLSRMSVQL 374
                                                                                                                                                                                         421 SLLSLYDNNIQ--SLANGTFDAMKSMKTVHL 449
                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98116655; PubMed=9455477;
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LRR_Cterm.
LRR_Nterm.
LRR_out.
                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
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                                                                                                                                                                                                                                                                                    STANDARD;
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IPR000483; L
IPR000372; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      FLRT2 OR KIAA0405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                    FLR2_HUMAN 043155;
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LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 ISTVELEDFKRYKELQRLGLGNNKITD - · IENGSLANIPRVREIHLENNKLKKIPSGLPE 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 NNKLTKI-HPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193 MNALHVLEMSANPLDNNGIEPGAF-EGVTVFHIRIAEAKLISVPKGLPPTLLELHLDYNK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLKLEELHLDDNSISTVGVEDGAFREAISLKLLFLSKNHLSSVPVGLPVDLQELRVDENR 191
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                             Transmembrane; Leucine-rich repeat; Repeat; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                   Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annoctation update)
Osteomodulin precursor (Osteoadherin) (OSAD) (Keratan sulfate
proteoglycan osteomodulin) (KSPG osteomodulin).
                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 660;
                                                                                                                                           EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                              LINKED (GLCNAC. . .) (P
9B15F283B0D5F778 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310 LKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVK 354
                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                            LRR 1.
LRR 2.
LRR 3.
LRR 4.
LRR 4.
LRR 6.
LRR 7.
LRR 7.
LRR 8.
LRR 8.
LRR 10.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                  62; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                        No. 1.9e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             423 AA
                                                                                                                                                                                                                                                                                                                                                                            15.7%; Score 313.5; 27.7%; Pred. No. 1.9
                                                                                                          POTENTIAL
                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                       74048 MW;
Pfam; PF00041; fn3; 1.
Pfam; PF00560; LRR; 8.
Pfam; PF01462; LRRWT; 1.
SMART; SM00370; LRR; 3.
SMART; SM00082; LRRCT; 1.
                                                                                  SMART; SM00369; LRR_TYP; 1.
                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 27.7
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                 musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                          521
660 AA;
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SEQUENCE FROM N.A.
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5542
5542
563
62
88
1132
1132
1183
2203
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035103;
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                              CARBOHYD
SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                  Ohno I., Matsubara K., Okubo K.; "The cloning and characterization of a cDNA for the novel bone matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Extracellular matrix; Proteoglycan;
Signal; Sulfation.
                                                                                                                                               Integrin (By similarity).
SUBUNIT: Binds the alpha(V)beta(3)-integrin (By similarity).
SUBCELLULAR LOCATION: Extracellular matrix (Potential).
TISSUE SPECIFICITY: Bone-specific.
PTM: Binds keratan sulfate chains (By similarity).
FTM: Sulfated on tyrosine residue(s) (By similarity).
FTM: SLIFATTY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS (SLRPS) FAMILY: CLASS II SUBFAMILY.
SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
                                                              protein; osteomodulin.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May be implicated in biomineralization processes:
function in binding of osteoblasts via the alpha(V)beta(3)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41ED7CA6B3A6F3B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC...) (N-LINKED (GLCNAC...) (M-LINKED (GLCNAC...) (
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BY SIMILARITY.
SULFATION (POTENTIAL).
SULFATION (POTENTIAL).
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POTENTIAL.
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LRR-S 1.
LRR-T 2.
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LRR-T 4.
LRR-T 4.
LRR-T 5.
LRR-T 6.
LRR-T 6.
LRR-T 6.
LRR-T 6.
LRR-T 7.
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InterPro; IPR001611; LRR.
InterPro; IPR001932; LRR_Usterm.
InterPro; IPR001892; LRR_out.
Pfam; PF00160; LRR; 10.
Pfam; PF01462; LRRNT; 1.
SWART; SM0013; LRRNT; 1.
Cell adhesion; Glycoprotein; Extr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB007848; BAA22790.1; -.
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278
316
423 AA;
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Gaps

66; Mismatches 134; Indels 21;

Dest Local Similaricy

38

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94 SVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKL--TKIHPKAFLTTKKL 151

Search completed: January 24, 2003, 12:25:53 Job time: 17 secs

317 VTMICPS 323

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GenCore version 5.1.3
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OM protein - protein search, using sw model

January 24, 2003, 12:22:00 Run on:

/ Search time 35 Seconds
(without alignments)
2231.196 Million cell updates/sec

1 MKEYVLLLFLALCSAKPFFS......PATFRCVLSRMSVQLGNFGM 379 US-09-944-457-2 1992 Perfect score: Sequence:

Title:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

671580 seqs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries

sp\_archea:\* sp\_bacteria:\* SPTREMBL\_21:\* Database :

sp\_vertebrate:\*
sp\_unclassified:\* sp\_fungi:\*
sp\_human:\*
sp\_invertebrate:\* sp\_rvirus:\*
sp\_bacteriap:\* sp\_mhc:\*
sp\_organelle:\* sp\_rodent:\* sp\_archeap: sp\_mammal:\* sp\_plant:\* sp\_virus:\* sp\_phage: \* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

o o	Description	aimordocaro 100000	O9nxp3 homo sapien	Q9de03 oreochromis	Q9ddz7 petromyzon	09ddz8 petromyzon	Q9de00 petromyzon	Q9ddz9 petromyzon	Q9de01 brachydanio	O9ctl6 mus musculu	094769 homo sapien	Q8wva2 homo sapien	Q9de02 brachydanio	Q9wvcl rattus norv	Q9y5q7 homo sapien	094813 homo sapien	09de36 brachydanio
SUMMARIES				~	7	m	0	Φ.	_	.0			~	_			.0
SOM	ID	090804	O9NXP3	09DE03	ZGG60	9ZQQ6Ö	09DE0	SZGG60	Q9DE01	O9CTL	094769	Q8WVA2	Q9DE02	Q9WVC1	Q9Y5Q7	094813	Q9DE36
	DB	-	4	13	13	13	13	13	13	11	4	4	13	11	4	4	13
	% Query Match Length DB	370	187	359	410	310	347	388	224	108	669	674	120	796	1525	1529	1512
	% Query Match	56.1	48.6	47.7	46.0	45.9	43.6	43.4	32.1	26.1	20.0	18.2	17.8	17.1	16.9	16.9	16.8
	Score	1118.5	968	950	917	915	869.5	865.5	638.5	520	397.5	363.5	354	340.5	336	336	335
	Result No.	1	7	m	4	J.	9	7	ω	6	10	11	12	13	14	15	16

	caeno	Q96k39 homo sapien	Q96kbl homo sapien	Q9p259 homo sapien	snm 6		095710 h	Q9wvb5 mus	075093	lrosc		a				Q9xyv4	Spweg 0		O75094 homo s	macaca	macac	Q8tf66 homo	P70193 mus	Q96ja1 homo sapien	OBbyb8 homo			Q92166 mus mus			Q9n4g6 caenorhabdi	Q9vpf0 drosophila	1 ratt	Q96dn1 homo sapien
	020204	Q96K39	Q96KB1	Q9P259	<b>09R1B9</b>	090WZ3	095710	Q9WVB5	075093	Q9V7F9	Q9WVB4	09V7F8	088280	088279	Q8WWZ2	<b>09XYV4</b>	Q9WUG5	Q9DE37	075094	Q9BGP6	Q95KI8	Q8TF66	P70193	Q96JA1	<b>09BYB8</b>	063156	Q9D3K0	09Z166	090XG4	Q8R5M3	Q9N4G6	Q9VPF0	070211	Q96DN1
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	1440	623	649	662	1521	1530	1521	1531	1534	1504	1523	1480	1523	1531	798	1504	1530	1515	1523	581	581	581	1091	1093	1094	96	391	1025	1095	578	542	1513	603	522
	10.7	16.6	16.6	16.6	16.6	16.6	16.5	16.5	16.5	16.4	16.3	16.3	16.3	16.2	16.1	16.1	16.0	15.6	15.5	15.3	15.3	14.9	14.9	14.5	14.5		14.2					13.9		•
	ν)	an.	m	331.5	(1)	331	329	329	328	326	325	324	324	323	320	320	319	311.5	309	304.5	304.5	297.5	296	289	289	287	282.5		282	281.5	28	276.5	276	275
1	/1	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	20

## ALIGNMENTS

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MEDLINE=20496956; PubMed=11040287;

MEDLINE=20496956; PubMed=11040287;

A Shintani S., Sato A., Toyosawa S., O'hUigin C., Klein J.;

Shintani S., Sato A., Toyosawa S., O'hUigin C., Klein J.;

A Shintani S., Sato A., Toyosawa S., O'hUigin C., Klein J.;

Ru Biglycan-like extracellular matrix genes of agnathans and teleosts.";

L. Mol. Evol. 51:363-373(2000).

R MEL: AFZ47821; AAG40156.1; -.

R InterPro; IPR001511; LRR.

InterPro; IPR001529; LRR. Mrerm.

InterPro; IPR003592; LRR. LRC.

InterPro; IPR003592; LRR. LYP.

R Ffam; PF00560; LRR.

R Ffam; PF001660; LRR.

SMART; SM00130: LRR.

SMART; SM00130: LRR.

SMART; SM00130: LRR.

SMART; SM00369; LRR. TYP; 5.

SEQUENCE 370 AA; 42177 MW; BCD0675694ECA2B7 CRC64;
                                                                                                                                                                        Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
Cichlidae; Oreochromis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.1%; Score 1118.5; DB 13; Length 370;
                                                        O9DE04;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Biglycan-like protein 3.
                                      370 AA.
                                        PRT;
                                      PRELIMINARY;
                                                                                                                                                                                                                                                   Cichlidae, Oreochromis.
NCBI_TaxID=8128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                      09DE04
RESULT 1
Q9DE04
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373 QLGNFGM 379 ||||||| 181 QLGNFGM 187

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qq

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EMBL; AK000136; BAA90967.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                   103 DITEIQQDDFKGLNKLYGLFLINNKISRIHPRAFKNMDNLRLLYLSYNMLNEIPANLPPN 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||:|:||::||:|| || ||:|||:|||| ||: ||:||||| ||: ||:||||| ||: ||:||||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: |
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                                                                                                                                                                                                                                                                                                                60 YND------EDCPAHCHCSPRVVQCSDQGLISVPDKIPEDTVMIDLQNN 102
                                                                                                                                                                                                                                                                                                                                                                                          112 KIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 TSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223 TSIPKDFPSSITELSLDYNKISKVEIEDFIRYKNLQRLGLAFNQIKYVENGSLANTPKIR 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 EIHLENNKLKKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNN 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 MNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKI 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 STVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSGLPELKY 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 STVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSGLPELKY 120
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                                            27; Gaps
                                                                                                                                                    1 MKEYVLLLFLALCSAKPFFSPSHIA--LKN------MMLKDMEDTDDDDDDDDDDDD 51.
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56.7%; Pred. No. 7e-72;
live 52; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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Pfam; PF00560; LRR; 3.
SEQUENCE 187 AA; 21074 MW; BDBEE37373CA3DBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNY-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ20129 fis, clone COL06190.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVKYWEMQPATFRCVLSRMSVQLGNF 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                        219; Conservative
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Matches 187; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
       Best Local Similarity
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                                        Matches
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MEDLINE_2046956; PubMed=11040287;
Shintani S., Sato A., Toyosawa S., O'hUigin C., Klein J.;
Shintani S., Sato A., Toyosawa S., O'hUigin C., Klein J.;
Shintani S., Sato A., Toyosawa S., O'hUigin C., Klein J.;
Biglycan-like extracellular matrix genes of agnathans and teleosts.";
J. Mol. Evol. 51:363-373(2000).
EMBL; AF247822; AAG40157.1; -.
InterPro; IPR001611; I.R.
InterPro; IPR001631; I.R.
InterPro; IPR003591; I.R.—Lyp.
Pfam; PF01462; IRRNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 PFDLFFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 PVIGGPKCPFRCQCHLRVIQCSDLGLKAVPEDIPDDTTLLDLQNNKITEIKENDFKNLKG 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 HLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306 GLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRC 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 LHALILVNNKLTIIHPKAFSPLTKLQRLYLSKNLLKEMPANMPKSLQELRIHENEITKIK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225 HLDGNKITKLTADRLKGMKNLAKLGLSYNQISSVENGTLSNAPHLRELHLDNNALTSVPP 284
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 359;
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                                                                                                                                                                                                                                                                                                          Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39807 MW; F149F9AA4E7572C6 CRC64;
                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.7%; Score 950; DB 13;
50.8%; Pred. No. 6.7e-60;
tive 57; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 410 AA.
                                                                         359 AA
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                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00370; LRR; 3.
SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_TYP;
                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cichlidae; Oreochromis
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VFDRSAIQLGNY 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                         09DE03
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Q9DDZ7
RESULT 3
                                    09DE03
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MEDLINE=20496956; PubMed=11040287; A Fibritani S., Sato A., Toyosawa S., O'hUigin C., Klein J.; Shiftani S., Sato A., Toyosawa S., O'hUigin C., Klein J.; Shiftani S., Sato A., Toyosawa S., O'hUigin C., Klein J.; Shiftani S., Sato S., Sato S., O'hUigin C., Klein J.; Lisas-373 (2000). The lisas-373 (2000). The lisas-373 (2000). The EMBL: ARZ47827; AAG40162.1; -. RinterPro; IPR001611; LRR_NErm.

R InterPro; IPR001519; LRR_NErm.

R InterPro; IPR001599; LRR_Lyp.

R InterPro; IPR001599; LRR_Lyp.

R Ffam; PF001660; LRR; 7.

R SMART; SM00013; LRR; 4.

R SMART; SM00013; LRRY; 1.

R SMART; SM00019; LRR_TYP; 8.
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MEDLINE=20496956; PubMed=11040287;
MEDLINE=20496956; PubMed=11040287;
Shinteni S., Sato A., Toyosawa S., O'huigin C., Klein J.;
Shinteni S., Sato A., Toyosawa S., O'huigin C., Klein J.;
"Biglycan-like extracellular matrix genes of agnathans and teleosts.";
J. Mol. Evol. 51:363-373(2000).
EMBL; AF247825; AAG40160.1; -.
InterPro; IPR001611; LR.
InterPro; IPR001592; LRR.
InterPro; IPR003592; LRR_Out.
InterPro; IPR003592; LRR_LYP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 LQVVYLHSNKIAAVKSDDFCSKGASPKRVLYSGISLFDNPVNYWDVPPSAFRCVASRSAV 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGM 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 NALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKI 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 STVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSGLPELKY 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313 LQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSV 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 CPFGCQCSARVVQCSDLGLVSVPQAIPKDARLLDLQNNKITEIKQDDFKGLNKLYALYLV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
                                                                                                                                                                                                                                                                                                                                                                           Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                               81; Indels
                                                                                                                                                                                                                                                                                                                                        310 AA; 34572 MW; 6FB8E05B14339EF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Biglycan-like protein 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                           45.9%; Score 915; DB 13;
56.2%; Pred. No. 1.7e-57;
tive 51; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 56.2*
Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                      SEQUENCE FROM N.A.
       NCBI_TaxID=7757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303 QFSQNF 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373 QLG-NF 377
                                                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
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                                                                                                                                                                                                            A MEDLINE-20466956; PubMed=11040287;

A Shintani S., Sato A., Toyosawa S., O'hUigin C., Klein J.;

A Shintani S., Sato A., Toyosawa S., O'hUigin C., Klein J.;

T Balgiyçan.-Ike extracellular matrix genes of agnathans and teleosts.";

L Mol. Evol. 51:363-373(2000).

R EMBL; AF247828; AAG40163.1; ...

R InterPro; IPR001311, LRR.

R InterPro; IPR00372; LRR_LOUt.

R InterPro; IPR00372; LRR_LOUt.

R InterPro; IPR003592; LRR_LOUt.

R InterPro; IPR003592; LRR_LOUt.

R InterPro; IPR003592; LRR_LOUt.

R InterPro; IPR003592; LRR_TYP.

R INTERPRO; IPR003592; LRR.

R SART; SM00370; LRR; 1.

BR SMART; SM00370; LRR; 1.

BR SMART; SM00370; LRR; 1.

BR SMART; SM00369; LRR_TYP; 8.

SEQUENCE 410 AA; 44671 MW; 3BC96E490BFCCEFA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 SVAPSATPKKVGGDRSKATAGKQPGRGAATPPKSLPPPPPPPPPPPASCPFGCQCSARVVQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 TTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 DNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKE 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIAR 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.0%; Score 917; DB 13; Length 410;
46.5%; Pred. No. 1.7e-57;
live 58; Mismatches 109; Indels 54; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 LLLVCALSSPSISSSVATATSSKPF-----55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 LLLFLAL------CSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDD 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SHFFPFDLFP------MCPFGCQCYSRVVH 86
                                                                                                         Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       326 VGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSVQLG-NF 377
               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Biglycan-like protein 2.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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BGL2.
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                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                NCBI_TaxID=7757;
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MEDIINE-20496956; Pubmed-11040287;
Shinteni S., Sato A., Toyosawa S., O'huigin C., Klein J.;
"Biglycan-like extracellular matrix genes of agnathans and teleosts.";
J. Mol. Evol. 51:363-373(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 NALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKI 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 STVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSGLPELKY 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 313 LQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSV 372
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         40 CPFGCQCSLRVVQCSDLGLKSVPASIPKDARMVDLQSNKITEIKQDDFKGLAQLHALFLV 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
NCBL_TaxID=7757;
                                                                                                                                                                                                                                                                                                                            1;
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                                                                                                                                                                                                                                                          DB 13; Length 347;
                                                                                                                                                                                                                                                                                                                            84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  388 AA; 42542 MW; 2E07169E9BB6071B CRC64;
                                                                                                                                                                 NON_TER 1 1
SEQUENCE 347 AA; 38266 MW; 55CC296938CED391 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
U-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Biglycan-like protein 1 (Fragment).
                                                                                                                                                                                                                                                              Score 869.5; DB 1
Pred. No. 3.4e-54;
                                                                                                                                                                                                                                       43.6%; Scc. No. ...
54.3%; Pred. No. ...
54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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InterPro; IPR001611; LRR.
InterPro; IPR003572; LRR_Nterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
Pfam; PF00560; LRR: 8
Pfam; PF01462; LRRNT; 1.
SMART; SM00370; LRRNT; 1.
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Pfam; PF00560; LRR; 8.
Pfam; PF01462; LRRNT; 1.
SMART; SM00370; LRR; 4.
SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_TYP; 6.
                                                                                                                                                                                                                                                                                                                            Matches 165; Conservative
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                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 HFGS 343
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                                                                                                                                                                                                                                                                                                  Local
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SEQUENCE FROM N.A.
MEDLINE-2046955; PubMed-11040287;
Shintani S., Sato A., Toyosawa S., O'hüigin C., Klein J.;
Shintani S., Sato A., Toyosawa S., O'hüigin G., Klein J.;
"Biglycan-like extracellular matrix genes of agnathans and teleosts.";
                   201 GRLHVIELGKNPLPSSGIEVGAFNGLDKLTYIRISYSKLTQLPKELPNSLLELHLEGNEI 260
                                                                                                                                                                                                                             253 STVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSGLPELKY 312
                                                                                                                                                                                                                                                                                                       313 LQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSV 372
                                                                                                                                                                                                                                                                                                                             94 SVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKRR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 LYLSHNOLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEP 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
                                                                           NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGM 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                       194 NALHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKI
                                                                                                                                                                                                                                                     261 VAIEDEDLFGYPYLFRLGLSYNKITEVQNGSLAVSGNLRELHLDNNLLVSVPPGLSKLRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 GAFEGV-TVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.1%; Score 638.5; DB 13; Length 224; 56.5%; Pred. No. 5.6e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 32.1%; Score 638.5; DB 13; Lengtn
Best Local Similarity 56.5%; Pred. No. 5.6e-38;
Matches 126; Conservative 37; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24442 MW; 54A1B7AB91667DF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Mol. Evol. 51:363-373(2000).
EMBL, AF247824; AAG40159.1; -
EFNB. 2DB-GENE-010105-1; dcn.
Interpro; IPR001611; LRR.
Interpro; IPR003592; LRR_out.
Interpro; IPR003591; LRR_typ.
Pfan; PF00560; LRR; TRR_TYP.
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SMART; SM00370; LRR; 5.
SMART; SM00369; LRR_TYP; 7.
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                                                                                                                                                                                                                                                                                                                                                                                   373 QLGN 376
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SEQUENCE
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Gaps

Matches 165; Conservative

Best Local Similarity

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Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=C7BL/65; TISSUE-EYEBALL;

KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Shibata K., Yoshino H., Adachi J., Fukuda S.,

A Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashurner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashurner M., Bealow G., Quackenbush J.,

Ruchil P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Ruski K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., Gasiboldi M.,

Ruskincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchioni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Scheenbach C., Seya T., Shibata Y., Storch K.-F.,

Nynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

R. Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 26.1%; Score 520; DB 11; Length 108; Best Local Similarity 84.2%; Pred. No. 6.3e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 AA; 12303 MW; 0BD4358D35949FFA CRC64;
             273 NNKITDIENGSLANIPRVREIHLENNKLKKIPSGLPELKYLQI 315
                                            :|:|: :|||||||:| :|||||| | :|:|| : ||:|| 182 HNEISVVENGSLANVPHLRELHLENNALTAVPAGLADHKYIQV 224
                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AKUZIJOU, MGD; MGD; MGI:1913945; ASpn.
InterPro: IPR000372; LRR_Nterm.
Pfam; PF01462; LRRNT; 1.
SWART; SM00013; LRRNT; 1.
NON TER 108 108
                                                                                                                                                                                                                                                                                                                               4631401G09Rik protein (Fragment).
ASPN OR 4631401G09RIK.
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EMBL; AK021386; BAB32393.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96; Conservative
                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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094769
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Q9CTL6
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SEQUENCE FROM N.A.

Mishiu J., Tanaka T., Nakamura Y.;

Tidentification of a novel gene (ECM2) encoding a putative

extracellular matrix protein expressed predominantly in adipose and

remale-specific tissues and its chromosomal localization to 9q22.3.";

Genomics 52:378-381(1998).

REMBL; AB011792; BAA33958 1;

REMBL; AB011792; BAA33958 1;

RICETPO; IPR001071; LRR.

RICETPO; IPR001071; VWF_C.

RICETPO; IPR001071; VWC; 1.

REMBL; SM0019; LEURICHRPT.

REMBL; SM00210; LEW; 4.

REMBL; SM00210; LWR; 1.

REMBL; SM00210; LWR; 1.

REMBL; SM00210; LWR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 QCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKLT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 K -- IHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGMNAL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 HVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKISTV 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --TDIENGSLANIP----- 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      501 TEICFNHTRKINVIVLRYNKIEENRIAPLAWINQENLESIDLSYNKLYHVPSYLPKSLLH 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289 -----RVREIHLENNKL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          561 LVLLGNQIERIPGYVFGHMEPGLEYLYLSFNKLADDGMDRVSFYGAYHSLRELFLDHNDL 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 KKIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 KDMEDTDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDFGC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148; Indels 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       699 AA; 79789 MW; E44E76A40A5C2742 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 74.1 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.0%; Score 397.5; DB 4 ilarity 24.9%; Pred. No. 3.1e-20; Conservative 77; Mismatches 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256 ELEDFKRYKELQRLGLGNNKI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01208; VWFC; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          680 YTFSCIRSYSSIVL 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                          NCBI_TaxID=9606;
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SEQUENCE 699
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O9WVC:
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EMBL; AF247823; AAG40158-1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 NALHVLEMSANPLDNNGIEPGAF-EGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKI 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 STVELEDFKRYKELQRLGLGNNKITD - · IENGSLANIPRVREIHLENNKLKKIPSGLPEL 310
                                                                                                                                                                                                                                                                                                                                                                                        74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                          134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGM 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    33;
                                                                                                                                                                                                                                                                                                                                     ch 18.2%; Score 363.5; DB 4; Length 674; 1 Similarity 32.7%; Pred. No. 7.8e-18; 92; Conservative 51; Mismatches 105; Indels 33;
                                             Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC018370, AAH18370.1; -
InterPro; IPR003961; FN__III.
InterPro; IPR004611; LRR.
InterPro; IPR004831; LRR_Cterm.
InterPro; IPR00372; LRR_Nterm.
InterPro; IPR00372; LRR_Nterm.
InterPro; IPR003121; PhospholipaseA2.
InterPro; IPR001211; LRR_TYP.
InterPro; IPR001211; LRR_TYP.
InterPro; IPR001011; LEURICHRPT.
                                                                                                                                                                                                                                                                                                                74087 MW; 38AB53F7243166CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Biglycan-like protein 3 (Fragment).
BGL3 OR BGL3.
Brachydanio rerio (Zebrafish) (Zebra danio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270 AHLQKLYLQDDAAISHIPYN----TLAKMRE--LERLDLSNN 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311 KYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNN 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 AA.
                                                                                                                                                                                                                                      SMART; SMO0370; LRR; 3.
SMART; SMO0082; LRRCT; 1.
SMART; SMO0013; LRRNT; 1.
PROSITE; PS00119; PA2_ASP; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                    Hypothetical protein. SEQUENCE 674 AA; 7
                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                          SEQUENCE FROM N.A.
NCBI_TaxID=9606;
                                       LISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                          Query Match
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Amargolia S.U.;

Amargolia Nonologues of the Drosophila slit protein are ligands of the heparan sulfate proteoglycan glypican-1 in brain.";

L. Biol. Chem. 274:17885-17892(1999).

EMBL: AF141386; AAD38440.2;

EMBL: AF141386; AAD38440.2;

InterPro: IPR001611; LRR.

InterPro: IPR0000483; LRR.Cterm.

InterPro: IPR000372; LRR.Cterm.

InterPro: IPR003592; LRR.Cterm.

InterPro: IPR003592; LRR.Lterm.

InterPro: IPR003592; LRR.Lterm.

InterPro: IPR003592; LRR.Lterm.

InterPro: IPR005692; LRR.Lterm.

InterPro: IPR005692; LRR.Lterm.

InterPro: IPR005929; LRR.Lterm.

INTERPRO: IPR006929; LRR.Ltr.

INTERPRO: IPR00692
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26.1%; Pred. No. 4.1e-16;
tive 55; Mismatches 120; Indels 139; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SPRAGUE DAWLEY;
MEDLINE-99292758; PubMed-10364234;
Liang Y., Annan R.S., Carr S.A., Popp S., Mevissen M., Margolis R.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 QNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----- 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 VPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VPKDIPANTLLLDLQNNDITEIKEDDFKGLDNLYALFLLNNQISKIHPKAFRNMDKLKIL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 YLSHNOLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.8%; Score 354; DB 13; Length 12
56.8%; Pred. No. 4.7e-18;
tive 26; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                       120 AA; 13569 MW; 37A302FB59F97696 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -MAY-2000 (TrEMBLrel. 13, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
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                                           InterPro; IPR001611; LRR.
InterPro; IPR003592; LRR.out.
InterPro; IPR003591; LRR.typ.
Pfam; PF00560; LRR; 4.
SMART; SM00370; LRR; 3.
SMART; SM00369; LRR; 3.
ZFIN; ZDB-GENE-010131-5; bgl3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 56.89 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 26.1
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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RESULT 15
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             169 PKSLAELR---IHENKVKKIQKDTFKGMNALHVLEMSANP-------LDNNGIE 212
                                         ---FEGVTVFH 223
                                                                              224 IRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELED-FKRYKELQRLGLGNNKITDIENG 282
                                                                                                                      SLANIPRVREIHLENNKLK----KIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKM 338
                                                                                                                                                           339 KKSLY------VLSRMS 371
                                                                                                                                                                        Brose K., Bland K.S., Wang K.H., Arnott D., Henzel W., Goodman C.S., Tessler-Laarigne M., Kidd T.;
"Slit proteins bind Robo receptors and have an evolutionarily conserved role in repulsive axon guidance.",
Cell 96:795-806(1999).
EMBL; AF133270; AAD255539.1; -.
                                                          456 TSGARCTSPRRLANKRIGQIKSKKFRCSGTEDYRSKLSGDCFADLACPEKCRCEGTTV--
                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99200389; PubMed-10102266;
Wang K.H., Brose K., Arnott D., Kidd T., Goodman C.S., Henzel W.,
                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                        PRT; 1525 AA
                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-BRAIN;
MEDLINE-99200391; Pubmed-10102268;
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InterPro; IPR000359; Cys_knot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cys_knot.
EGF-like.
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InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
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EGF_Ca.
Foln.
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Pfam; PF00054; laminin_G; 1.
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                                                                                                                                                                                                                                                                        PRELIMINARY;
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InterPro; IPR001881;
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                                       213 -PGA----
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MEDIINE-99033071; PubMed-9813312;
IIOh A., Miyabbayahi T., Ohno M., Sakano S.;
"Cloning and expressions of three mammalian homologues of drosophila
slit suggest possible roles for slit in the formation and maintenance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               573 AFEGASGVNEILLTSNRLENVQHKMFKGLESLKTL---MLRSNRITCVGNDSF-----I 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 SNNQISELAPDAFQGLRSLNSLVLYGNKITELPKSLFEGLFSLQLLLLNANKINCLRVDA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 PKSLAELR---IHENKVKKIQKDTFKGMNALHVLEMSANP------LDNNGIE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----FEGVTVFH 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 IRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELED-FKRYKELQRLGLGNNKITDIENG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283 SLANIPRVREIHLENNKLK----KIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKM 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 16.9%; Score 336; DB 4; Length 1525; Best Local Similarity 26.5%; Pred. No. 1.9e-15; Matches 105; Conservative 61; Mismatches 120; Indels 110; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 QNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNL 168
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00302; LRR; 6.

SMART; SM00082; LRRCT; 4.

SMART; SM00082; LRRCT; 4.

SMART; SM000013; LRRTY; 4.

RESIDENCY SM000869; LRR TYP; 8.

RESIDENCY SM00086; LRR TYP; 8.

RESIDENCY SM000086; LRR TYP; 8.

RESIDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-UNU-2002 (TrEMBLrel. 21, Last annotation update)
Slit-2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          339 KKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSVQL 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   624 GLSSVRLLSLYDNQIT--TVAPGAFDTLHSLSTLNL 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1529 AA
                                                                                                                                                          CT; 1.
EGF_CA; 2.
EGF_like; 7.
FOLN; 2.
LamG; 1.
                                                       PF01463; LRRCT; 4. PF01462; LRRNT; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                     SMART; SM00041; C
SMART; SM00179; E
SMART; SM00011; E
SMART; SM00274; F
SMART; SM0282; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
PF00560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 -PGA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       094813
                                                       Pfam;
                                                                                                              Pfam;
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Fri Jan 24 13:09:55 2003

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HSSP; P00740; IEDM.
ZFIN; ZDB-GENE-010306-3; slit2.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000359; Cys knot.
InterPro; IPR000561; EGF-1ike.
                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001881; BGF_Ca.
InterPro; IPR001438; BGF_II.
InterPro; IPR002645; F01N.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR001791; Laminin_G.
                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000483; LRR_Cterm.
InterPro; IPR00372; LRR_Nterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
Pfam; PF00008; EGF; 9.
Pfam; PF00054; laminin_G; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00010; EGFBLOOD.
PRINTS; PR00011; EGFLAMININ.
PRINTS; PR00019; LEURICHRPT.
                                                                                                                                                                                                                        Yeo S.Y., Okamoto H.; "Zebrafish slit2 homolog.";
                                                                                                                                                                                                                                                                                                                                                 IPR000742; EGF_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                IPR001611; LRR.
                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01463; LRRCT; 4.
Pfam; PF01462; LRRNT; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00560; LRR; 18
                                                                                                                                                    Cyprinidae; Danio.
                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                 NCBI_TaxID=7955;
                                                                                                                                                                                                            STRAIN-MICHIGAN;
                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; I
InterPro; I
                                                                                                                                                                                                                                                                                                                                                 InterPro;
                 Q9DE36
  09DE36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 16.9%; Score 336; DB 4; Length 1529; Best Local Similarity 26.0%; Pred. No. 1.9e-15; Matches 105; Conservative 61; Mismatches 120; Indels 118; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDT-------RMLDL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 QNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169 PKSLAELR---IHENKVKKIQKDTFKGMNALHVLEMSANP------LDNNGIE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 FEGVIVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELED-FKRYKELQRLGLGNN 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KITDIENGSLANIPRVREIHLENNKLK----KIPSGLPELKYLQIIFLHSNSIARVGVND 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 SNNQISELAPDAFQGLRSLNSLVLYGNKITELPKSLFEGLFSLQLLLLNANKINCLRVDA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           452 TSGARCTSPRRLANKRIGQIKSKKFRCSAKEQYFIPGTEDYRSKLSGDCFADLACPEKCR 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               512 CEGTTV---DCSNQKLNKIPEHIPQYTAELRLNNNEFTVLEATGIFKKLPQLRKINFSNN 568
                                                                                                                                                                                                                                                                                                                                          SMART; SW00282; Lamid; 1.

SMART; SW00370; LRR; 6.

SMART; SW003082; LRRCT; 4.

SMART; SW00013; LRRNT; 4.

SMART; SW00013; LRRNT; 4.

SMART; SW00013; LRR TYP; 8.

R PROSITE; PS01185; CTCK_1; UNKNOWN_1.

R PROSITE; PS01185; CTCK_2; 1.

R PROSITE; PS01186; EGF_1; UNKNOWN_9.

R PROSITE; PS01187; EGF_1; UNKNOWN_9.

R PROSITE; PS01187; EGF_1; GF CA, 2.

CALCIUM-DIAding; EGF_11ke domain; Glycoprotein; Repeat.

SEQUENCE 1529 AA; 169869 MW; 5D19CC5E7FD461BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | : | : | : |
F-----IGLSSVRLLSLYDNQIT--TVAPGAFDTLHSLSTLNL 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 FCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSVQL 374
of the nervous system.";
Brain Res. Mol. Brain Res. 62:175-186(1998).
EMBL; AB017168; BAA35185.1; -.
                                        HSSP; P00743; 1CCF.
InterPro; IPR000152; Asx_hydroxyl.
                                                                  InterPro; IPR000359; Cys_kkot.
InterPro; IPR000561; EGF-like.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR003645; FolN.
InterPro; IPR001791; Laminin_G.
                                                                                                                                                              InterPro; IPR000483; LRR_Cterm.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
                                                                                                                                                                                                                                                                                       SMART; SM00041; CT; 1.
SMART; SM00179; EGF_CA; 2.
SMART; SM00001; EGF_1ike; 7.
SMART; SM00274; FOLN; 2.
SMART; SM00282; LamG; 1.
                                                                                                                                                                                                                     PF00008; EGF; 9.
PF00054; laminin_G; 1.
                                                                                                                                                      InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                Pfam; PF00560; LRR; 17.
Pfam; PF01463; LRRCT; 4.
Pfam; PF01462; LRRNT; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 ----
                                                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         626
  Q
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RESULT 16

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12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PRSHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDT------- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 POSHSSCSVL--QCPELCTCSNNVVDCRGKGLTEIPTNLP-ETITEIRLEQNSIKIIPAG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 -----RMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRLY 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 16.8%; Score 335; DB 13; Length 1512; Best Local Similarity 27.1%; Pred. No. 2.2e-15; Matches 110; Conservative 61; Mismatches 129; Indels 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS00022; EGF_1; UNKNOWN_9.
PROSITE; PS01186; EGF_2; 8.
PROSITE; PS01187; EGF_CA; 2.
SEQUENCE 1512 AA; 166669 MW; 60888COAFOC3D630 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF210321; AAG36773.1; -.
                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0019; LEURICHRFT.
SMART; SM00101; CT; 1.
SMART; SM00101; GCF_CA; 9.
SMART; SM001019; EGF_CA; 9.
SMART; SM00001; EGF_CA; 9.
SMART; SM00001; EGF_LIKE; 6.
SMART; SM00274; FOLN; 2.
SMART; SM00027; LERE; 14.
SMART; SM00010; LRRE; 14.
SMART; SM001013; LRRUT; 4.
SMART; SM001013; LRRUT; 4.
SMART; SM001013; LRRUT; 4.
SMART; PS000101; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS01185; CTCK_1; UNKNOWN_1.
                                                                                                                                                                                                                                               Brachydanio rerio (Zebrafish) (Zebra danio).
PRT; 1512 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
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156 LSHNQLSEIPLNLPKSLAELR---IHENKVKKIQKDTFKGMNALHVLEMSANP----- 205
                  216 ----FEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELED-FKRYKELQRL 269
                                                                                                                                      430 KWLADYLQDNPIETSGARCTSPRRLANKRIGQIKSKKFRCSGVEDYRSKLGGDCFADLAC 489
                                                                                                                                                                             270 GLGNNKITDIENGSLANIPRVREIHLENNKLKKIP-SGLPELKYLQIIFLHSNSIARVGV 328
                                                                                                                                                                                                         547 NLSNNKITDIEEGTFEGASGVNELILTSNRLEGVHYSMLKGLGGLRTLMLRSNRISCVNN 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                       329 NDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSVQL 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                           607 GSFTGL-----SSVRLLSLYDNLIT--SMSPGAFDTLHSLSTLNL 644
                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                  PRT; 1440 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP, P00740; JEDM.
InterPro; JPR000152; Asx_hydroxyl.
InterPro; JPR000059; Cys_knot.
InterPro; JPR0000561; EGF-1ike.
InterPro; JPR001881; EGF_2.
InterPro; JPR001881; EGF_Ca.
InterPro; JPR001438; EGF_II.
InterPro; JPR001439; Laminin_G.
InterPro; JPR001431; Laminin_G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Z69792; CAA93668.2; -. AL022270; CAA93668.2; JOINED. AL022270; CAB63434.1; -.
                                                         206 -----LDNNGIE-PGA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z69792; CAB63434.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000483; LRR_Cterm.
InterPro; IPR000372; LRR_Nterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
Pfam; PF00008; EGF; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01463; LRRCT; 4.
Pfam; PF01462; LRRNT; 4.
PRINTS; PR00010; EGFBLOOD.
                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00560; LRR; 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   investigating biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         F40E10.4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                       F40E10.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smye R
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                                                                                                                                                                                                                                                                                                                  RESULT 17
Q20204
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                                                                                                                                                                                                                                                                                      317 DLSKNIITEIQPKAFLGLHNLHTLVLYGNNITDLKSDTFEGLGSLQLLLLNANQLTCIRR 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
CDNA FLJ14788 fis, clone NT2RP400925, weakly similar to fibromodulin
                                                                                                                                                                                                                            74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
                                                                                                                                                                                                                                                                                                                                                                                                                   191 KGMNALHVLEMSANP---LDNNGI-----------EP--GAFEGVTVFH-- 223
                                                                                                                                                                                                                                                                                                                                      137 QGPEFLEVLNLDKNHIFCLENNVISSWVSLEVLTLNGNRLTTFEEPSNARFRQLDLFNNP 196
                                                                                                                                                                                                                                                                                                                                                                                197 WNCDCRLRWMRKWLEKAEGONKTVCATPLNLQGSSIEILQDKFMTCSGNRKRRYKKTCET 256
                                                                                                                                                                                                                                                                                                                                                                                                       -----LTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRL 269
                                                                                                                                                                                                                                                                                                                                                                                                                                               270 GLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSGLPE-LKYLQIIFLHSNSIA--RV 326
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                 16.7%; Score 332.5; DB 5; Length 1440; 26.5%; Pred. No. 3.1e-15; tive 57; Mismatches 126; Indels 117;
    327 GVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSVQL 374
                                                                                                                                                                                                                                                                                                                                                             --IRIAEAK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    623 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
LEURICHRPT.
                                                                                                                                                                                            Best Local Similarity 26.5% Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
PR00019;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   precursor.
                                                                                                                                                                                   Query Match
PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               096K39;
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us-09-944-457-2.rspt

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Q9P259
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A ISOGAIT. Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

A ISOGAIT. Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

A Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara M.,

A Wagatsuma M., Hosoiri T., Kaku Y., Koddira H., Kondo H., Sugawara M.,

A Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

A Mananoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

A Minomiya K., Iwayanagi T.;

A Mananoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

A Minomiya K., Iwayanagi T.;

A Ninomiya K., Iwayanagi T.;

B Pfam; PF00040; I.RR.

B Pfam; PF00146; I.RR.

B Pfam; PF01463; I.RRCT; I.
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01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
CDNA FLJ14391 fis, clone HEMBA1003077, weakly similar to SLIT protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253 STVELEDFKRYKELQRLGLGNNKITDIENGS--LANIPRVREIHLENNKLKKIPSGLPEL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGM 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 NALHVLEMSANPLDNNGIEPGAFEGVTVFHIR-IAEAKLTSVPKGLPPTLLELHLDYNKI 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 NAGI----PSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRTITYDSLSKI 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 STISSPSLQGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGT 221
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                              27;
                                                                                                                                                                                                                                                                                                                                                ch 16.6%; Score 331.5; DB 4; Length 623; 1 Similarity 33.0%; Pred. No. 1.3e-15; 86; Conservative 37; Mismatches 111; Indels 27
                                                                                           ### PF0041; file | 1...

Pfam; PF00560; LRR; 10...

Pfam; PF01463; LRRT; 1...

Pfam; PF01462; LRRT; 1...

SMART; SM00013; LRRT; 1...

PROSITE; PS00119; PA2_ASP; UNKNOWN_1...

PROSITE; PS00119; PA2_ASP; UNKNOWN_1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   649 AA.
                 Interpro; IPR000483; LRR_Cterm.
Interpro; IPR000372; LRR_Nterm.
Interpro; IPR001211; PhospholipaseA2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
InterPro; IPR001611; LRR
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74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
                                                                                                                                                                                                                                                                                                                                                                                                                            72 NAGI----PSDLKNLLKVERIXLXHNSLDEFPTNLPKYVKELHLQENNIRTITYDSLSKI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 PYLEELHLDDNSVSAVSIEEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 STVELEDFKRYKELQRLGLGNNKITDIENGS--LANIPRVREIHLENNKLKKIPSGLPEL 310
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                       134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGM 193
                                                                                                                                                                                                                                                                                                                               31 CPSVCRCDAGFIYCNDRFLTSIPTGIPEDATTLYLQNNQI------------------771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XVII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";

EMBL; AB040902; BAA95993.1; -.
InterPro; IRP003961; FN_III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 NALHVLEMSANPLDNNGIEPGAFEGVTVFHIR-IAEAKLTSVPKGLPPTLLELHLDYNKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                      27;
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                                                                                                                                        Query Match
16.6%; Score 331.5; DB 4; Length 649;
Best Local Similarity 33.0%; Pred. No. 1.4e-15;
Matches 86; Conservative 37; Mismatches 111; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   662 AA; 74459 MW; FF7CCCE689E4B429 CRC64;
SMART; SMO0060; FN3; 1.
SMART; SMO013; LRRNT; 1.
PROSTIE; PS00113; PA2_ASP; UNKNOWN 1.
SEQUENCE 649 AA; 72994 MW; 820B527E53F62F08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) KIAA1469 protein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 331.5;
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Interpro; IPR000372; LRR_Nterm.
Interpro; IPR003592; LRR_Cterm.
Interpro; IPR003591; LRR_typ.
Interpro; IPR001211; PhospholipaseA2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-20277482; Pubmed-10819331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311 KYLQIIFLHSNSIARVGVNDF 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 N-LRKLYLQDNHINRVPPNAF 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.6%;
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Pfam; PF00560; LRR: 10.
Pfam; PF01463; LRRCT: 1.
Pfam; PF01462; LRRNT: 1.
SMART; SM00060; FN3; 1.
SMART; SM00370; LRR: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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090WZ3;
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                                                                                                                                                                                                                                                                                        141 PYLEELHLDDNSVSAVSIEEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRI 200
                                                                      74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
                                                                                                                                                                                                                                                               194 NALHVLEMSANPLDNNGIEPGAFEGVTVFHIR-IAEAKLTSVPKGLPPTLLELHLDYNKI 252
                                                                                                                                                                                                                                                                                                                                                           STVELEDFKRYKELQRLGLGNNKITDIENGS--LANIPRVREIHLENNKLKKIPSGLPEL 310
                                                                                                                                                                                                                                                                                                                                                                                                        201 STISSPSLOGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGT 260
                                                                                                                                                                  134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGM 193
                      27; Gaps
                                                                                                                44 CPSVCRCDAGFIYCNDRFLTSIPTGIPEDATTLYLONNOI-------N 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yuan W., Zhou L., Chen J.H., Wu J.Y., Rao Y., Ornitz D.M.;
"The mouse SLIT family: secreted ligands for ROBO expressed in
patterns that suggest a role in morphogenesis and axon guidance.";
Dev. Biol. 212:290-306(1999).

EMBL, ARI44628; AAD44759.1; -.
HSSP; P00743; ICCF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
1 Similarity 33.0%; Pred. No. 1.4e-15;
86; Conservative 37; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1521 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000152; Asx. hydroxyl.
InterPro; IPR000359; Cys_knot.
InterPro; IPR000359; Cys_knot.
InterPro; IPR000742; EGF_2.
InterPro; IPR0019481; EGF_Ca.
InterPro; IPR001741; EGF_Ca.
InterPro; IPR001791; Laminin_G.
InterPro; IPR001791; Laminin_G.
InterPro; IPR001791; Laminin_G.
InterPro; IPR001791; Laminin_G.
InterPro; IPR000483; LRR_Cterm.
InterPro; IPR000781; LRR_Cterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=SWISS WEBSTER/ICR;
MEDLINE=99365246; PubMed=10433822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 KYLQIIFLHSNSIARVGVNDF 331
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SMART; SM00179; EGF_CA; 2.
SMART; SM00001; EGF_like; 7.
SMART; SM00274; FOLN; 2.
SMART; SM00282; LamG; 1.
SMART; SM00370; LRR; 6.
SMART; SM00082; LRRCT; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01463; LRRCT; 4.
Pfam; PF01462; LRRNT; 4.
PRINTS; PR00019; LEURICHRPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00054; laminin_G; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:1315205; Slit2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00008; EGF; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00560; LRR; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
Best Local
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09R1B9
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Q9R1B9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 QNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 PKSLAELR---IHENKVKIQKDTFKGMNALHVLEMSANP-------LDNNGIE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : | | : :::||:: : | || : |: :: || 392 FQDLHNLNLLSLYDNKLQTVAKGTFSALRAIQTMHLAQNPFICDCHLKWLADYLHTNPIE 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 -PGA-----FEGVTVFH 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                452 TSGARCTSPRRLANKRIGQIKSKKFRCSGTEDYRSKLSGDCFADLACPEKCRCEGTTV-- 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 IRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELED-FKRYKELQRLGLGNNKITDIENG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283 SLANIPRVREIHLENNKLK----KIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKM 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       339 KKSLY------VLSRMS 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       626 LLSLYDNQITTVAPGAFDSLHSLSTLNLLANP------FNCNCHLAWLGEWLRRKR 675
                                                                                                                                                                                                                                                                                                                                                                  16.6%; Score 331.5; DB 11; Length 1521;
25.6%; Pred. No. 3.9e-15;
Live 56; Mismatches 121; Indels 139; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----RMLDL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE-99200392; PubMed-10102269;
Li H., Chen J.-H., Wu W., Fagaly T., Zhou L., Yuan W., Dupuis S., Jiang Z., Nash W., Gick C., Ornitz D.M., Wu J.Y., Rao Y.;

"Vertebrate slit, a secreted ligand for the transmembrane protein roundabout, is a repellent for olfactory bulb axons.";
Cell 96:807-818(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
SWART; SW00013; LRRNT; 4.

SWART; SM00369; LRR_TYP; 8.

PROSITE; PS001010; ASX_HYDROXYL; UNKNOWN_2.

PROSITE; PS01125; CTCK_2; 1.

PROSITE; PS01186; EGF_1; UNKNOWN_9.

PROSITE; PS01186; EGF_2; 7.

PROSITE; PS01187; EGF_2; 7.

Calcium-binding; EGF-like domain; Glycoprotein; Repeat.

SEQUENCE 1521 AA; 168769 MW; 97DCA36157897884 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Rao Y., Li H., Wu J.Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1530 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDT--
                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       676 IVTGN 680
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74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDT------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        623 SVRMLSLYDNQIT--TVAPGAFDTLHSLSTLNL 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               342 LYSAISLFNNPVKYWEMQPATFRCVLSRMSVQL 374
                                                                                                                                         interPro; IPR000152; Asx_hydroxyl.
                                                                                                                                                             InterPro; IPR000359; Cys_knot.
InterPro; IPR000561; BGF-like.
InterPro; IPR000742; BGF_2.
InterPro; IPR001881; BGF_Ca.
InterPro; IPR001881; BGF_Ca.
InterPro; IPR0013645; FolN.
                                                                                                                                                                                                                                                                                     InterPro; IPR000483; LRR_Cterm.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
Pfam; PF00008; EGF; 9.
                                                                                  Mech. Dev. 79:57-72(1998).
EMBL; AF055585; AAD04309.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00054; laminin_G; 1.
Pfam; PF00560; LRR; 17.
                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01463; LRRCT; 4.
Pfam; PF01462; LRRNT; 4.
SMART; SM00041, CT; 1.
SMART; SM00179; EGF_CA; 2.
SMART; SM0001; EGF_1Ke; 7.
SMART; SM00274; FOLN; 2.
SMART; SM00282; LamG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00369; LRR_TYP; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00082; LRRCT; 4.
SMART; SM00013; LRRNT; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 101; Conservative
                                                                                                                                                                                                                                                                            InterPro; IPR001611;
                                                                                                                          P00743; 1CCF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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                                                               organogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341 SNNQISEIAADAFQGLRSLNSLVLYGNKITELPKGLFEGLFSLQLLLLNANKINCLRVDS 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401 FQDLHNLNLLSLYDNKLQTIAKGTFSPLRAIQTLHLAQNPFICDCHLKWLADYLHTNPIE 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 -PGA------FEGVTVFH 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 IRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELED-FKRYKELQRLGLGNNKITDIENG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                             16.6%; Score 331; DB 13; Length 1530;
26.8%; Pred. No. 4.3e-15;
tive 60; Mismatches 120; Indels 110; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----- 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          461 TSGARCTSPRILANKRIGQIKSKKFRCSGTEDYRSKLSGDCFADLACPEKCRCEGTTV-- 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283 SLANIPRVREIHLENNKLK----KIPSGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKM 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 519 -DCSNOKLTKIPDHIPQYTAELRLNNNEFTVLEATGIFKKLPQLRKINLSNNKITDIEEG 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            578 AFEGANGVNELLLTSNRMENVRHKMFKGLEGLKTL---MLRSNHISCVNNDSFTGL---- 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE-KIDNEY, AND BRAIN;
MEDLINE-99279238; PubMed-10349621;
Holmes G.P., Negus K., Burridge L., Raman S., Algar E., Yamada T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Neurogenic extracellular SLIT protein SLIT2.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                         PÉGMI; PF00008; BGF; 9.

PÉGMI; PF00054; laminin_G; 1.

PÉGMI; PF000560; LRR.; 17.

PÉGMI; PF01462; LRRUT; 4.

PÉGMI; PF01462; LRRUT; 4.

PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_2.

PROSITE; PS01125; CTCK_1; UNKNOWN_1.

PROSITE; PS01125; CTCK_2; 1.

PROSITE; PS01186; EGF_1; UNKNOWN_9.

PROSITE; PS01186; EGF_2; UNKNOWN_2.

PROSITE; PS01186; EGF_2; UNKNOWN_2.

PROSITE; PS01186; EGF_2; UNKNOWN_2.

PROSITE; PS01186; AGF_2; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 PKSLAELR---IHENKVKKIQKDTFKGMNALHVLEMSANP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  339 KKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSVQL 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       631 -- SSVRLLSLYDNQIT--TVAPGAFDTLHSLSTLNL 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1521 AA.
EMBL; AY046070; AAL02123.1; -.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000359; Cys_knot.
InterPro; IPR000561; EGF-like.
InterPro; IPR001742; EGF_2.
InterPro; IPR001781; IGR_G.
InterPro; IPR001791; Iaminin_G.
InterPro; IPR001791; IRR_Cterm.
InterPro; IPR000483; IRR_Cterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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095710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       510 -DCSNQKLNKIPEHIPQYTAELRLNNNEFTYLEATGIFKKLPQLRKINFSNNKITDIEEG 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 SLANIPRVREIHLENNKLKKIPSGL-PELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKS 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----- 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 PKSLAELR---IHENKVKKIQKDTFKGMNALHVLEMSANP------LDNNGIE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         392 FQDLHNLNLLSLYDNKLQTIAKGTFSPLRAIQTMHLAQNPFICDCHLKWLADYLHTNPIE 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------FEGVTVFH 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      452 TSGARCTSPRRLANKRIGQIKSKKFRCSGTEDYRSKLSGDCFADLACPEKCRCEGTTV-- 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 IRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELED-FKRYKELQRLGLGNNKITDIENG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        569 AFEGASGVNEILLTSNRLENVQHKMFKGLEKPQNLMLRSNRITCVGNDSF-----IGLS 622
"Distinct but overlapping expression patterns of two vertebrate slit homologs implies functional roles in CNS development and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.5%; Score 329; DB 4; Length 1521; 25.7%; Pred. No. 5.9e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00022; EGF_1; UNKNOWN_9.
PROSITE; PS01186; EGF_2; 7.
PROSITE; PS01187; EGF_CA; 2.
Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
SEQUENCE 1521 AA; 168947 WW; C05A0DF7D78C48C9 CRC64;
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01-NOV-1998 (TrEMBLrel. 08, 01-AUG-1999 (TrEMBLrel. 11, 01-DEC-2001 (TrEMBLrel. 19,
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Pfam; PF01463; LRRCT; 4.
Pfam; PF01462; LRRNT; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Slit-1 protein. SLIT-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                339 KKSLY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         075093;
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25.5%; Pred. No. 6e-15;
tive 62; Mismatches 116; Indels 114; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 QNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEI---P 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDT----------RMLDL 108
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIM-SWISS WEBSTER/ICR;
MEDLINE-93165246, pubMed=10433822;
Yuan W., Zhou L., Chen J.H., Wu J.Y., Rao Y., Ornitz D.M.;
The mouse SLIT family: secreted ligands for ROBO expressed in patterns that suggest a role in morphogenesis and axon guidance.";
Dev. Biol. 212:290-306 (1999).
EMBL; AF144627; AAD44758.1;
HSSP; PO0743; ICCF.
                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---
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Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
SEQUENCE 1531 AA; 167546 MW; F7D09AA6693A4F30 CRC64;
                                                                                                                                  Last sequence update)
Last annotation update)
                                                         PRT; 1531 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM0369; LRR_TYP; 10.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_2.
PROSITE; PS01185; CTCK_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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PROSITE; PS00022; EGF_1; UNKNOWN_9.
PROSITE: PS01186; EGF_2; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1315203; Slitl.
InterPro; IPR000152; Asx.hydroxyl.
InterPro; IPR000359; Cys_knot.
InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000742; EGF_2.
InterPro; IPR01881; EGF_Ca.
InterPro; IPR01881; EGF_Ca.
InterPro; IPR001848; EGF_II.
InterPro; IPR001791; Laminin_G.
InterPro; IPR001791; Laminin_G.
InterPro; IPR001791; LRR.
InterPro; IPR000372; LRR_Oterm.
InterPro; IPR003592; LRR_Oterm.
InterPro; IPR003592; LRR_Oterm.
InterPro; IPR003591; LRR_Oterm.
InterPro; IPR003591; LRR_Oterm.
Pfam; PP00008; EGF; 9.
Pfam; PP000084; IRR_OTERM.
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SWART; SM00179; EGF_CA; 2.
SWART; SM00001; EGF_like; 7.
                                                                                                 01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00010; EGFBLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00282; LamG; 1.
SMART; SM00370; LRR; 3.
SMART; SM00082; LRRCT; 4.
SMART; SM00013; LRRUT; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00560; LRR; 19.
Pfam; PF01463; LRRCT; 4.
Pfam; PF01462; LRRNT; 4.
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                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM00274; FOLN; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                NCBI_TaxID-10090;
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                                                      Q9WVB5
                                                                                 Q9WVB5
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RESULT 24
Q9WVB5
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RX MEDLINE-99033071; PubMed-9813312; RA ItCh A., Miyabayashi T., Ohno M., Sakano S.; Altoh A., Miyabayashi T., Ohno M., Sakano S.; Altoh A., Miyabayashi T., Ohno M., Sakano S.; Itch A., Miyabayashi T., Sakano S., Mol. Bain Res. 62:175-186(1998).

B. Marain Res. Mol. Bain Res. 62:175-186(1998).

B. MiterPro; IPR00139; EGF_1.

B. MiterPro; IPR00143; EGF_1.

B. MiterPro; IPR00143; EGF_1.

B. MiterPro; IPR00143; Laminin_GGF.

B. MiterPro; IPR00144; Laminin_GGF.

B. MiterPro; IPR00145; Laminin_GF.

B. MiterPro; IPR00145; Laminin_GF.
341 SNNQIAEIAPDAFQGLRSLNSLVLYGNKITDLPRGVFGGLYTLQLLLLNANKINCIRPDA 400
                                                                              166 LNLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANP------LDNNGIE 212
                                                                                                                              224 ---IRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELED-FKRYKELQRLGLGNNKITDI 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280 ENGSLANIPRVREIHLENNKLKKIPSGL-PELKYLQIIFLHSNSIARVGVNDFCPTVPKM 338
                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1534 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----SAISLFNNP 352
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PRINTS; PRO0011; EGFLAMININ.
SWART; SM00041; CT; 1.
SWART; SM00179; EGF_CA; 2.
SWART; SM00201; EGF_LIKe; 7.
SWART; SM00224; FOLN; 3.
SWART; SM00282; LamG; 1.
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; Pred. No. 7e-15; 70; Mismatches 121; Indels 104; Gaps 12;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                            Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Ii P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Prannkood C., Baldwin D., Beallew R.M., Basson A., Barandal J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341 SNNQIAEIAPDAFQGLRSLNSLVLYGNKITDLPRGVFGGLYTLQLLLLNANKINCIRPDA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 LNLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANP------LDNNGIE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --PGAFE---- 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                461 TSGARCASPRRLANKRIGQIKSKKFRCSAKEQYFIPGTEDYQLNSECNSDVVCPHKCRCE 520
                                                                                                                                                                                                                                                                                                                                                                ----- 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           581 EDGAFEGAASVSELHLTANQLESIRSGMFRGLDGLRTLMLRNNRISCIH-NDSFTGLRNV 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224 ---IRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELED-FKRYKELQRLGLGNNKITDI
                                                                                                                                                                                                                                                                          16.5%; Score 328; DB 4; Length 1534; 25.5%; Pred. No. 7e-15;
SMART; SM00082; LRRCT; 4.

SMART; SM00013; LRRNT; 4.

SMART; SM00013; LRRNT; 4.

SMOOTH SM0013; LRRNT; 4.

PROSITE; PS01185; CTCK_1; UNKNOWN_2.

PROSITE; PS01185; CTCK_2; 2.

PROSITE; PS01186; EGF_2; 8.

PROSITE; PS01186; EGF_CA; 2.

PROSITE; PS01186; EGF_CA; 2.

PROSITE; PS01187; EGF_CA; 2.

PROSITE; PS01184; EGF_CA; 2.

PROSITE; PS01187; EGF_CA; 3.

PROSITE; PS01187; EGF_CA; 3.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
SLI protein.
SLI protein.
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                                                                                                                                                                                                                                                                                                                                                                     74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDT------
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MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                         Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                 Similarity
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RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Diactz S.M.,
A Dodson K., Doup L.E., Downes M. Dugan-Rocha S., Dunkov B.C.,
Dunn P.,
RA Dodson K., Doup L.E., Downes M. Dugan-Rocha S., Dunkov B.C.,
Dunb R.A Glodek A., Gong F., Gerrel J.M., Glasser K.,
RA Glodek A., Gong F., Gerrell J.H., Glaz., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wein H.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.K., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Nelson D.L.,
RA Spier E., Spradling A.C., Standers R.D.C., Scheeler F., Shen H.,
RA Spier E., Standling A.C., Standers R.D.C., Scheeler F., Smith T.,
RA Spier E., Standling A.C., Standers B., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Weinstock G.M., Weissenbach J.,
RA Zheng X.H., Zhong W., Zhong W., Zhong G., Zhao Q., Zheng X.,
Ry Gibbs R.A., Myers E.W., Rubin G.M., Venter E., Smith H.O.,
RA Zheng X.H., Zhong W., Zhong W., Zhong S., Zhu X., Smith H.O.,
RR Shelp Pool/All Elby W., Rubin G.M., Venter J.C.;
RR Schence 287:2185-2195(2000).
RR Schence 287:2185-2195(2000).
RR Schence Sequence of Drosophila melanogaster.";
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PROSITE; PS01186; BGF_2; 5.
PROSITE; PS01187; BGF_CA; 2.
PROSITE; PS01187; BGF_CA; 2.
PROSITE; PS01187; BGF_1 | Ref domain; Glycoprotein; Hydroxylation; Repeat.
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25.7%; Pred. No. 9.5e-15;
Live 55; Mismatches 124; Indels 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1504 AA; 168597 MW; 836A3F5022BF234F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIVBase; regulatorizz, circulatorizz, InterPro; IPR000152; Asx_hydroxyl. InterPro; IPR000359; Cys.knot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGF_2.
EGF_Ca.
Laminin_EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; irrogos; cys.—interPro; irrogos; cys.—interPro; irrogos; cys.—interPro; irrogos; cys.—interPro; irrogos; cys.—interPro; irrogos; cys.—interPro; irrogos; ir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS01185; CTCK_1; 1. PS01225; CTCK_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGF_like; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00011; EGFLAMININ PRINTS; PR00019; LEURICHRPT
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SMART; SM00370; LIRR; 4.
SMART; SM00082; LRRCT; 4.
SMART; SM00013; LIRRNT; 4.
SMART; SM00369; LIR_TYP; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBase; FBgn0003425; sli.
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SMART; SM00179; EGF_CA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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PROSITE;
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74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133

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13 CPRVCSCTGLNVDCSHRGLTSVPRKISADVERLELQGNNLTVIYETDFQRLTKLRMLQLT 132
                                                   134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNL---PKSLAELRIHENKVKKIQKDTF 190
                                                                     || :| |:
193 KGAQSLRSLQ-----LDNNQITCLDEHAFKGLVELEILTLNNNNLTSLPHNIFGGLGRLR 247
                                                                                                                                                                                                                                                                   308 HAPMECGAENSCPHPCRCADGIVDCREKSLTSVPVTLPDDTTELRLEQNFITELPPKSFS 367
                                                                                                                                                                                                                                                                                                                 262 RYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSGL-PELKYLQIIFLHS 320
                                                                                                                                                                                                                                                                                                                                  368 SFRRLRRIDLSNNNISRIAHDALSGLKQLTTLVLYGNKIKDLPSGVFKGLGSLQLLLLNA 427
                                                                                                                                                                                                                248 ALRLSDNPFACDCHLSWLSRFLRSATRLAPYTRCQSPSQLKGONVADLHDQEFKCSGLTE 307
                                                                                                                                                                                                                                                   -----EAKLTSVPKGLPPTLLELHLDYNKISTVELEDFK 261
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SEQUENCE FROM N.A.

MEDLINE-99365246; Pubmed-10433822;

Yuan W., Zhou L., Chen J.H., Wu J.Y., Rao Y., Ornitz D.M.;

The mouse SLIT family: secreted ligands for ROBO expressed in graterns that suggest a role in morphogenesis and axon guidance.";

Dev. Biol. 212:290-306(1999).

EMBL; AF144629; AAD44760.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                               321 NSIARVGVNDFCPTVPKMKKSLY--SAISLFNNPVKYWEMQPATFRCVLSRMSVQL 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                   ------RIA-----
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                                                                                                                191 KGMNALHVLEMSANPLDNNGI---EPGAFEGVTVFHI-
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InterPro; IPR001881; EGF 2.
InterPro; IPR001438; EGF II.
InterPro; IPR002400; GF cysknot.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR001791; Laminin_G.
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MGD; MGI:1315202; S1143.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000359; Cys_knot.
InterPro; IPR000561; EGF-like.
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InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_out.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00008; EGF; 9. Pfam; PF00054; laminin_G; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01463; LRRCT; 4.
Pfam; PF01462; LRRNT; 4.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR00011; EGFLAMININ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKS---LAELRIHENKVKKIQKDTF 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1:1 :1: :
209 TLRLHSNHLYCDCHLAWLSDWLRQRRTIGQFTLCMAPVHLRGFSVADVQKKEYVCPGPHS 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       329 QYKKLKRIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITTEIPKGLFDGLVSLQLLLLNA 388
                                                                                                                                                                                                                                                                                                                                                                                                                     74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 CPTKCTCSAASVDCHGLGLRAVPRGIPRNAERLDLDRNNITRITKMDFAGLKNLRVLHLE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----HIR---IAEAK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 KGMNALHVLEMSANPLDNNG---IEPGAFEG-------VTVF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BERKELEY;
MEDLINE-20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
                                                                                                                                                                                                                                                                                                                                               Ouery Match 16.3%; Score 325; DB 11; Length 1523; Best Local Similarity 25.4%; Pred. No. 1.1e-14; Matches 100; Conservative 59; Mismatches 111; Indels 124;
                            SWART; SM00041; CT; 1.

SWART; SM00019; EGF_CA; 1.

SWART; SM00179; EGF_CA; 1.

SWART; SM00012; LamG; 1.

SWART; SM00370; LRR; 7.

SWART; SM0036; LRRCT; 4.

SWART; SM00136; LRR_TYP; 7.

SWART; SM00169; LRR_TYP; 7.

SWART; SM00169; LRR_TYP; 7.

PROSITE: PS01010; ASX HYDROXYL; UNKNOWN_1.

PROSITE: PS01125; CTCK_2; 1.

R PROSITE: PS01125; CTCK_2; 1.

R PROSITE: PS01186; EGF_1; 7.

R PROSITE: PS01187; EGF_2; 7.

PROSITE: PS01187; EGF_2; 7.

R PROSITE: PS01187; EGF_2; 7.
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SEQUENCE 1523 AA; 167711 MW; F43A3F3E016C4BFC CRC64;
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Last sequence update)
Last annotation update)
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                  LEURICHRPT.
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2002 (TrEMBLrel. 21,
PR00438; GFCYSKNOT.
PR00019; LEURICHRPT
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SLI OR CG8355.
PRINTS; F
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Q9V7F8
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Abernacy R.A., Henders S.E., Richards S.D., Ashbunner W., Henderson S.N., Schrich S.C., Herman S.E., Richards S.E., Ashbunner W., Children B.D., Man K.L., Doyle C.C., Hearter E.C., Beld C.C., Medson C.R., Making C.B., Abbildia J.E., Morges Y. H., Can Blades P. G. Chinger M. Pfeldicfer B.D. Man K.L., Doyle C.C., Barter E. C., Beld C. Medson C.R., Milking G.L.G., Ballow D. Bolshor D. Ballow D. Bolshor S.W., Ballow D. Bolshor D. Bolshor S.W., Ballow D. Bolshor S.W., Ballow D. Bolshor S.W., Barter S. M., Borkel J., Boyletter P. Borkove S., M. Borkove S., M. Borkove D., Bolchan M. R., Bouck J., Brofstein P., Borther P. W., Chandra I., Borther S.W., Ballow D. Bolshor D. Bolshor S.W., Carley S., Dohlke C., Dowenport, L.B., Davies P. M., Carley S., Dohlke C., Dowenport, L.B., Davies P. M., Carley S., Dohlke C., Dowenport, L.B., Davies P. M., Carley S., Dohlke C., Dowenport, L.B., Davies P. M., Carley S., Dohlke C., Dowenport, L.B., Davies P. M., Carley S., Dohlke C., Dowenport, L.B., Davies P. M., Man M., M., Carley S., M., Carley S., Carley S., Calbart W. M., Glasser K., M., Marchis M. K., Brongelista C.C., Ferrara C., Eerrara C., Eerr

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Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat. SEQUENCE 1480 AA; 165888 MW; F456BC617D8453ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDT-------RMLDLQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 AEAKLTSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGGNNKITDIENGSLAN 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309 REKSLTSVPVTLPDDTTELRLEQNFITELPPKSFSSFRRLRRIDLSNNNISRIAHDALSG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          369 LKQLTTLVLYGNKIKDLPSGVFKGLGSLQLLLLNANEISCIRKDAF------RDLHSL 420
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                 73 CPRVCSCTGLNVDCSHRGLTSVPRKISADVERLELQGNNLTVIYETDFQRLTKLRMLQLT 132
                                                                                                                                                                                                                                                                                                                                                                                                               110 NNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLP 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 -----FEGVTVFHIRI 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287 IPRVREIHLENNKLKKIPSGL-PELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLY-- 343
                                                                                                        16.3%; Score 324; DB 5; Length 1480; 25.8%; Pred. No. 1.3e-14; Indels 104; Gaps iive 63; Mismatches 123; Indels 104; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Makayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
"Identification of high-molecular-weight proteins with multiple EGF-like motifs by motif-trap screening.";
EMBL; AB011531; BAA32461.1; -.
HSSP; P01153; LEGF-
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000159; Asx_hydroxyl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 KSLAELRI---HENKVKKIQKDTFKGMNALHVLEMSANPL------
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN; MEDLINE=98360089; PubMed=9693030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GF_cysknot.
Laminin_G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000372; LRR_Nterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
Pfam; PF00008; EGF; 9.
Pfam; PF00054; laminin_G; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRR_Cterm.
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EGF-like.
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                                                                                                                                                                                      Matches 101; Conservative
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                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                Query Match
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641 LESLYDNHITTISPGAFDTLQALSTLNLLANP 672
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                                                                                                                                                                                                                                                                                                                                                                                    269 EAPACNANSLSCPSACSCSNNIVDCRGKGLTEIPANLPEGIVEIRLEQNSIKSIPAGAFI 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
                                                                                                                                                                                                                                                                                74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLFSLYGLILN 133
                                                                                                                                                                                                                                                                                                                           134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKS---LAELRIHENKVKKIQKDTF 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSGLPE-LKYLQIIFLHS 320
                                                                                                                                                                                                                                  16.3%; Score 324; DB 11; Length 1523; 25.4%; Pred. No. 1.3e-14; tive 59; Mismatches 111; Indels 124; Gaps
                                                                                                                                                                                                                                                                                             34 CPTKCTCSAASVDCHGLGLRAVPRGIPRNAERLDLDRNNITRITKMDFTGLKNLRVLHLE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-SPRAGUE-DAWLEY, TISSUE-BRAIN;
MEDLINE-98360089; PubMed-9693030;
Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
"Identification of high-molecular-weight proteins with multiple EGF-
                                                                                                                                                                                                                                                                                                                                                                       191 KGMNALHVLEMSANPLDNNG---IEPGAFEG--------VTVF-----
                                                                                                                              PROSITE; PS00010. ASK_HYDROXYL; UNKNOWN_2.
PROSITE; PS01185; CTCK_1; UNKNOWN_1.
PROSITE; PS01205; CTCK_2; 1.
PROSITE; PS01205; EGF_1; UNKNOWN_9.
PROSITE; PS01186; EGF_2; 7.
PROSITE; PS01187; EGF_CA; 2.
Calcium-binding; EGF_1ke domain; Glycoprotein; Repeat.
SEQUENCE 1523 AA; 167767 WW; 6CE1B7AF9244478E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               389 NKINCLRVNTF-----QDLQNLNLLSLYDNKLQ 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 NSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVK 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1531 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                         SMART; SM00041; CT; 1.
SMART; SM00179; EGF_CA; 1.
SMART; SM0001; EGF_like; 8.
SMART; SM00282; LamG; 1.
SMART; SM00370; LRR; 5.
SMART; SM00082; LRRCT; 4.
SMART; SM00013; LRRNT; 4.
SMART; SM0013; LRRNT; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 08, C
(TrEMBLrel. 08, I
(TrEMBLrel. 19, I
                               PRINTS; PR00438; GFCYSKNOT
                                                                                                                                                                                                                                                         Matches 100; Conservative
PF00560; LRR; 19.
PF01463; LRRCT; 4.
PF01462; LRRNT; 4.
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SEQUENCE FROM N.A.
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01-NOV-1998 (
01-DEC-2001 (
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282 CPAMCSCSNGIVDCRGKGLTAIPANLP-ETMTEIRLELNGIKSIPPGAFSPYRKLRRIDL 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 ---IRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELED-FKRYKELQRLGLGNNKITDI 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 16.2%; Score 323; DB 11; Length 1531; Best Local Similarity 25.0%; Pred. No. 1.6e-14; Matches 98; Conservative 64; Mismatches 116; Indels 114; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 QNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEI---P 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 LNLPKSLAELRIHENKVKKIOKDTFKGMNALHVLEMSANP-------LDNNGIE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 ENGSLANIPRVREIHLENNKLKKIPSGL-PELKYLQIIFLHSNSIARVGVNDFCPTVPKM 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R Pfam; PF0030; LRKT; 19.

R Pfam; PF01463; LRRCT; 4.

R PFAM; PF01463; LRRCT; 4.

R PRINTS; PR00101; EGFBLOOD.

R SMART; SM00179; EGF_CA; 2.

R SMART; SM00074; FOLM: 3.

R SMART; SM00024; Folm: 3.

R SMART; SM000370; LRR; 3.

R SMART; SM00019; LRR; 3.

R SMART; SM00019; LRR; 3.

R SMART; SM00019; LRRYT; 4.

R SMART; SM00019; LRRTY; 4.

R SMART; SM00019; LRR_TYP; 10.

R PROSITE; PS01109; ASX_HYDROXYL; UNKNOWN_1.

R PROSITE; PS01185; CTCK_1; UNKNOWN_1.

R PROSITE; PS01187; EGF_C3; 1.

R PROSITE; PS01187; EGF_C3; 2.

R PROSITE; PS01187; EGF_C4; 2.
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like motifs by motif-trap screening.";
Genomics 51:27-34(1998).
                                                                                                                                                                                      Interpro; 1PR000152; Asx_hydroxyl.
Interpro; 1PR000559; Cys_knot.
Interpro; 1PR000551; EGF-11ke.
Interpro; 1PR000542; EGF-2.
Interpro; 1PR001881; EGF_2.
Interpro; 1PR001481; EGF_1.
Interpro; 1PR001481; EGF_1.
Interpro; 1PR001481; IRR.
Interpro; 1PR001611; IRR.
Interpro; 1PR0001611; IRR.
Interpro; 1PR000483; IRR_Cterm.
Interpro; 1PR000483; IRR_Nerm.
Interpro; 1PR000592; IRR_Nerm.
Interpro; 1PR003592; IRR_Nerm.
Interpro; 1PR003592; IRR_Nerm.
Interpro; IPR003592; IRR_Nerm.
                                                                                                          EMBL; AB011530; BAA32460.1; -. HSSP; P00743; 1APO.
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Fri Jan 24 13:09:55 2003

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::: | :: | :: | | :: | | 385 KINCIRPDAFQDLQNLSLLSLYDNKIQSLAKGTFTSLRAIQTLHLAQNPFICDCNLKWLA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 -FDTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHN 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 QLSEI---PLNLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANP------ 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----GV 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               445 DFLRTNPIETSGARCASPRRLANKRIGQIKSKKFRCSAKEQYFIPGTEDYQLNSECNSDV 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 TVFH-----IRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELED-FKRYKELQRLG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   505 VCPHKCRCEANVVECSSLKLTKIPERIPQSTAELRLNNNEISILEATGMFKKITHLKKIN 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 LGNNKITDIENGSLANIPRVREIHLENNKLKKIPSGL-PELKYLQIIFLHSNSIARVGVN 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 565 LSNNKVSEIEDGAFEGAASVSELHLTANQLESIRSGMFRGLDGLRTLMLRNNRISCIH-N 623
                                                                                                                                                                         Teasdale R.D., Rumballe B., Georgas K., Yamada T., Little M.H.;
"Conserved modularity, size and potential for alternate splicing in
all three human Slit genes";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL. AVC92183, AAX31796.1;
InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR_Cterm.
InterPro; IPR000483; LRR_Cterm.
InterPro; IPR0003592; LRR_Out.
InterPro; IPR003592; LRR_Out.
Pfam; PF01463; LRR_T; 15.
Pfam; PF01463; LRRCT; 3.
                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                         16.1%; Score 320; DB 4; Length 798; 24.7%; Pred. No. 1.2e-14; Indels 112; ive 69; Mismatches 124; Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88906 MW; 1A9094A414BABD04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSVQL 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : :: | : : | : | : | DSFTGLRNVR-----LLSLYDNQIT--TVSPGAFDTLQSLSTLNL 661
                                                                01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                798 AA.
                                                     Created)
                                PRT;
                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0019; LEURICHRPT.
SWART; SM00370; LRR: 11
SWART; SM00082; LRRCT; 3.
SWART; SM00013; LRRUT; 4.
SWART; SM00369; LRR_TYP; 16.
                                                    01-MAR-2002 (TrEMBLrel. 20,
                                                                                    SLIT1 isoform B (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                               PRELIMINARY;
                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                    798 AA;
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                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                           NCBI_TaxID=9606;
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SEQUENCE
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Best Local 3
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Q9XYV4
         RESULT 31
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6
                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99200390; PubMed=10102267;
Kidd T., Bland K.S., Goodman C.S.;
"Slit is the midline repellent for the robo receptor in Drosophila.";
cell 96:785-794(1999).
EMBL: AF126540; AAD26567.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNL---PKSLAELRIHENKVKKIQKDTF 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 KGAOSLRSLO----LDNNOITCLDEHAFKGLVELEILTLNNNNLTSLPHNIFGGLGRLR 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.1%; Score 320; DB 5; Length 1504; 25.2%; Pred. No. 2.5e-14; tive 57; Mismatches 124; Indels 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00022; EGF_1; UNKNOWN_7.
PROSITE: PS01186; EGF_2; 5.
PROSITE: PS01187; EGF_2, 2.
Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
SEQUENCE 1504 AA; 168569 WW; A377D3BAACBIC743 CRC64;
                                                                                        01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 KGMNALHVLEMSANPLDNNGI ---EPGAFEGVTVFHI
PRT; 1504 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_3.
PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01225; CTCK_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flybases; Fepronous, 25, 511.
InterPro; IPR000152; 8xz.hydroxyl.
InterPro; IPR000359; Cys_knot.
InterPro; IPR000561; EGF-like.
InterPro; IPR000742; EGF-2.
InterPro; IPR001742; EGF-2.
InterPro; IPR001749; Laminin_EGF.
InterPro; IPR001791; Laminin_G.
InterPro; IPR001791; Laminin_G.
InterPro; IPR001751; LRR_Cterm.
InterPro; IPR000752; LRR_Cterm.
InterPro; IPR000359; LRR_Cterm.
InterPro; IPR0003591; LRR_Cterm.
InterPro; IPR0003591; LRR_Cterm.
InterPro; IPR0003591; LRR_Ttp.
Pfam; PF00064; Iaminin_G; 1.
Pfam; PF001463; LRRCT; 4.
Pfam; PF01462; LRRNT; 4.
PRINTS; PR00019; EGFLAMININ.
PRINTS; PR00019; LGRLAMININ.
                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00041; CT; 1.
SMART; SM00179; EGF_CA; 2.
SMART; SM00001; EGF_LIKe; 5.
                                                         01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00282; LamG; I. SMART; SM00370; LRR; 4 . SMART; SM00082; LRRCT; 4 . SMART; SM00013; LRRNT; 4 . SMART; SM00013; LRRNT; 4 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBqn0003425; sli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 105; Conservative
   PRELIMINARY;
                                                                                                                                                  SLIT protein.
SLI OR SLIT OR CG8355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7227;
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AND STUDENT FROM W. T. B. WARD K. B. WEDLINE-99200391; PubMed=10102268; Brose K., Bland K.S., Wang K.H., Arnott D., Henzel W., Goodman C.S., Brose K., Bland K.S., Wang K.H., Arnott D., Henzel W., Goodman C.S., Brose K., Bland K.S., Wang K.H., Arnott D., Henzel W., Goodman C.S., Stranger C., Bland R., Kalda T.; Sit proteins bind Robo receptors and have an evolutionarily and proteins bind Robo receptors and have an evolutionarily can graph of 1975-80 (1999).

R. Call 96:795-80 (1999).

R. BMBL, AF13730; AAD25540.1; -. BRBL, AF13730; AAD25540.1; -. BRBL, AF13730; BCF-1ike.

DR. InterPro; IPR000152; BCF-1ike.

DR. InterPro; IPR001438; BCF-11.

DR. InterPro; IPR001438; BCF-11.

DR. InterPro; IPR001749; Laminin_EGF.

DR. InterPro; IPR00161; Laminin_GG.

DR. InterPro; IPR000483; LRR_Cterm.

DR. InterPro; IPR000483; LRR_Cterm.

DR. InterPro; IPR000391; LRR_Cterm.

DR. InterPro; IPR000391; LRR_Cterm.

DR. InterPro; IPR00088; EGF.

DR. InterPro; IPR00088; EGF.

DR. InterPro; IPR00088; EGF.

DR. InterPro; IPR00088; EGF.
                                248 ALRLSDNPFACDCHLSWLSRFLRSATRLAPYTRCQSPSQLKGQNVADLHDQEFKCSGLTE 307
                                                                                                                                          262 RYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSGL-PELKYLQIIFLHS 320
                                                                                                                                                               308 HAPMECGAENSCPHPCRCADGIVDCREKSLTSVPVTLPDDTTDVRLEQNFITELPPKSFS 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                    -----EAKLTSVPKGLPPTLLELHLDYNKISTVELEDFK
                                                                                                                                                                                                                 321 NSIARVGVNDFCPTVPKMKKSLY--SAISLFNNPVKYWEMQPATFRCVLSRMSVQL 374
                                                                                                                                                                                                                                  428 NEISCIRKDAF------RDLHSLSLLSLYDNNIQ--SLANGTFDAMKSIKTVHL 473
                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00041; CT; 1.
SMART; SM00179; EGF_CA; 2.
SMART; SM00179; EGF_Like; 7.
SMART; SM00274; FGLN; 2.
SMART; SM00274; FGLN; 2.
SMART; SM00730; LRR; 5.
SMART; SM00082; LRRC; 4.
SMART; SM00083; LRRCT; 4.
SMART; SM00013; LRRUT; 4.
SMART; SM0013; LRRUT; 4.
SMART; SM0013; LRRUT; 4.
PROSITE; PS00118; CTCK_1; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                PRT; 1530 AA.
-----RIA----
                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00008; EGF; 9.
Pfam; PF00054; laminin_G; 1.
Pfam; PF00156; LRRC1; 18.
Pfam; PF01463; LRRC1; 4.
Pfam; PF01462; LRRN1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00010; EGFBLOOD.
PRINTS; PR00011; EGFLAMININ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00019; LEURICHRPT
                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
                                                                    228 -----
                                                                                                                                                                                                                                                                                                                                              Q9WUG5
                                                                                                                                                                                                                                                                                                        RESULT 33
Q9WUG5
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                                                                                                                                                                                    341 SNNQIAEIAPDAFQGLRSLNSLVLYGNKITDLPRGVFGGLYTLQLLLLNANKINCIRPDA 400
                                                                                                                                                                                                                                                                                                                 280 ENGSLANIPRVREIHLENNKLKKIPSGL-PELKYLQIIFLHSNSIARVGVNDFCPTVPKM 338
                                                                                                         Ouery Match 16.0%; Score 319; DB 11; Length 1530;
Best Local Similarity 25.0%; Pred. No. 3.1e-14;
Matches 98; Conservative 63; Mismatches 117; Indels 114; Gaps
                                                                                                                                                                                                                                  109 ONNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEI---P 165
                                                                                                                                                                                                                                                                                               166 LNLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANP------LDNNGIE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLIT3.
Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                        224 ---IRIAEAKLTSVPKGLPPTLLELHLDYNKISTVELED-FKRYKELQRLGLGNNKITDI
                                                                                                                                                                                                                                                                                                                                                                                                                                          461 TTGARCASPRRLANKRIGQIKSKKFRCSAKEQYFIPGTEDYHLNSECTSDVACPHKCRCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF210320; AAG36772.1; -.
HSSP; P0740; LDD.
ZFIN; ZDB-GENE-010306-4; slit3.
InterPro; IPR000152; Asx_bydroxyl.
InterPro; IPR000159; Cys_knot.
InterPro; IPR000561; EGF-like.
InterPro; IPR001791; EGF-2.
InterPro; IPR001891; EGF-2.
InterPro; IPR001891; EGF_Ca.
InterPro; IPR001891; Laminin_G.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS00022; EGF_1; UNKNOWN_9.
PROSITE; PS01186; EGF_2; 8.
PROSITE; PS01187; EGF_CA:
Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
SEQUENCE 1530 AA; 167385 MW; 622A510E9ACC9B5F CRC64;
                                                                                                                                                                                                                                                                                                                                                         -----EEGVTVFH------
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1515 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  339 KKSLY-----SAISLFNNP 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
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LRR_Nterm.
LRR_out.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=MICHIGAN;
Yeo S.Y., Okamoto H.;
"Zebrafish slit3 homolog.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                             213 -PGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000483;
InterPro; IPR000372;
InterPro; IPR003592;
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Query Match
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                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                     74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
                                                                                                                                                                                                                                                                                                                             134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKS---LAELRIHENKVKKIQKDTF 190
                                                                                                                                                                                                                                                                                                                                        226 ------INSVPKGLPPTLLELHLDYNKISTVELEDFKRY 263
                                                                                                                                                                                                                                             15.6%; Score 311.5; DB 13; Length 1515; 23.9%; Pred. No. 1e-13; tive 63; Mismatches 114; Indels 123; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           217 ----- 225
                                                                                                                                                                                                                                                                                                                                                                                                                              202 IHSNNIHCDCHLSWLSDWLRQRRGLAPFTQCMAPAHMRGLNVPDVQKREFVCTGPVETEP 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                              | : : | | : | | : | | 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 KELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSGLPE-LKYLQIIFLHSNS 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 CPHKCSCSGSHVDCQGQAFKTVPRGIPRNAERLDLDRNNITRITKVDFSGLKNLRVLHLE 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                   M00369; LREATYP; 18.
PS00010; ASX HYDROXYL; UNKNOWN_1.
PS01185; CTCK_1; UNKNOWN_1.
PS0125; CTCK_2; 1.
PS00022; EGF_1; UNKNOWN_9.
PS01186; EGF_2; 7.
PS01187; EGF_CA; 2.
1515 AA; 166871 MW; 12FD111277D18D5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                323 IARVGVNDFCPTVPKMKKSL--YSAISLFNNPVK 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              382 INCLRVNTF-----KDLQNLNLLSLYDNKLQ 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1523 AA
                                                                                                                                                                                                                                                                                                                                                                    191 KGMNALHVLEMSANPLDNNGIEPGAF------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=99033071; PubMed=9813312;
InterPro; IPR003591; LRR_typ. Pfam; PF00008; EGF; 9. Pfam; PF00054; laminin_G; 1.
                                                                    SMART; SM00041; CT; 1.
SMART; SM01181; EGF; 9.
SMART; SM00179; EGF_CA; 8.
SMART; SM00001; EGF_Iike; 6.
SMART; SM00282; LamG; 1.
                              Pfam; PF00560; LRR; 18-
Pfam; PF01463; LRRCT; 4.
Pfam; PF01462; LRRNT; 4.
PRINTS; PR00019; LEURICHRPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, 01-AUG-1999 (TrEMBLrel. 11, 01-AUG-1992 (TrEMBLrel. 21, SLIT-3 protein (MEGF5).
                                                                                                   SMART; SM00001; EGF_like; 6
SMART; SM0282; LamG; 1.
SMART; SM00370; LRR; 14.
SMART; SM00082; LRRCT; 4.
SMART; SM00013; LRRNT; 4.
SMART; SM00019; LRRTYP; 18
                                                                                                                                                                                                                                                        Best Local Similarity 23.9:
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                     SMART; SM
PROSITE;
                                                                                                                                                                         PROSITE;
PROSITE;
PROSITE;
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                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                       PROSITE;
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  δλ
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                                                            slit suggest possible roles for Slit in the formation and maintenance of the nervous system.";
Brain Res. Mol. Brain Res. 62:175-186(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 RGITDVKNLQ-----LDNNHISCIEDGAFRALRDLEILTLNNNNISRILVTSFNHMPKIR 208
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Itoh A., Miyabayashi T., Ohno M., Sakano S.; "Cloning and expressions of three mammalian homologues of Drosophila
                                                                                                                                                                                                                                                                           Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.; "Identification of high-molecular-weight proteins with multiple EGF-like motifs by motif-trap screening."; Genomics 51:27-34(1998).
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Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
SEQUENCE 1523 AA; 167684 MW; 52549041D1D6DBD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00370; LRR; 4.
SMART; SM00082; LRRCT; 4.
SMART; SM00013; LRRCT; 4.
SMART; SM00369; LRR_TYP; 9.
PROSITE; PS001010; ASK_MYDROXYL; UNKNOWN_2.
PROSITE; PS01125; CTCK_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00022; EGF_1; UNKNOWN_9. PROSITE; PS01186; EGF_2; 7. PROSITE; PS01187; EGF_CA; 2. PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000152; Asx_hydroxyl.
                                                                                                                                                                                                                                                 MEDLINE=98360089; PubMed=9693030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR001791; Laminin_G.
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                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB017169; BAA35186.1; -. EMBL; AB011538; BAA32466.1; -.
                                                                                                                                                                                        SEQUENCE OF 785-1523 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000359; Cys_knot.
InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01463; LRRCT; 4.
Pfam; PF01462; LRRNT; 4.
PRINTS; PR00011; EGFLAMININ.
PRINTS; PR00019; LEURICHRPT.
SMART; SM00141; CT; 1.
SMART; SM00179; EGF_CA; 1.
SMART; SM0001; EGF_LIKe; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003592; IRR_out.
InterPro; IPR003591; IRR_typ.
Pfam; PF00008; EGF; 9.
Pfam; PF00054; Iaminin_G; 1.
Pfam; PF00560; IRR; 19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P00740; 1EDM.
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231 LONLYLQWNKISVIG----QTMSWTWSSL-QRLDLSGNEIEAFS-GPSVFQCVPNLQRL 283
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284 NL 285
                                                                 371 SV 372
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284 NL 285
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Osada N., Halda M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
Suguki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQIIPLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCV--LSRM 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 NALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKIS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----KLLSLHLRSNSLR 170
                                                                        269 EPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIVEIRLEQNSIKAIPAGAFT 328
                                                                                                                                                                                                                 74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
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                                    ---LTSVPKGLPPTLLELHLDYNKISTVELEDFK 261
                                                                                                                                                                      262 RYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSGLPE-LKYLQIIFLHS 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 65.9 kDa protein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           libraries.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB056426; BAB33084.1; -.
InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR_Cterm.
InterPro; IPR000483; LRR_Cterm.
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SEQUENCE 581 AA; 65895 MW; A025CF13AA663730 CRC64;
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                                                                                                                                                                                                                                                                                                                                                   389 NKINCLRVNTF-----QDLQNLNLLSLYDNKLQ 416
                                                                                                                                                                                                                                                                                                            321 NSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVK 354
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01-JUN-2001 (TIEMBLIEL 17, Last seq
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InterPro; IPR003591; LRR_typ.
Pfam; PF00560; LRR; 9.
Pfam; PF01463; LRRCT; 1.
Pfam; PF01462; LRRNT; 1.
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SM00369; LRR_TYP; 9.
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Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCV--LSRM 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 NALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKIS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 TVELEDFKRYKELORLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSGL-PELKY 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 19, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 65.9 kDa protein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Macaca imetacos, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.3%; Score 304.5; DB 6; Length 581; 28.8%; Pred. No. 1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Libraries.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB060846; BAB46888.1;
ThterPro: IPR001611; LRR.
InterPro: IPR000483; LRR_Cterm.
InterPro: IPR000483; LRR_Cterm.
R Pfan; PP00560; LRR; 9.
R Pfan; PP01462; LRRCT; 1.
R Pfan; PF01462; LRRUT; 1.
R SMRRT; SM00013; LRRUT; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              581 AA; 65880 MW; 8E4F1BBD043669BF CRC64;
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581 AA.
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                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=TEMPORAL LOBE RIGHT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
PRELIMINARY;
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Satoh K., Hata M., Yokota H.; "A Novel Member of the Leucine-Rich Repeat Superfamily Induced in Rat Astrocytes by beta-Amyloid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 TFKGMNALHVLEMSANPLDNNGIEPGAFE---GVT-------VFH----- 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 IRIAEAKLTSVPKG-------LPP-----TLLELHLDYNKISTVE 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 PSIFWQLPQLNRLTLFGNSLKELSLGIFGPMPNLRELWLYDNHISSLPDNVFSNLRQLQV 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   322 LILSRNQISFISPGAFNGLTELRELSLHTNALQDLDGNVFRMLANLQNISLQNNRLR--Q 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 LNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPK---SLAELRIHENKVKKIQKD 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 HFSQCSNLKELQLHGNHLEY - IPDGAFDHLVGLTKLNLGKNSLTHISPRVFQHLGNLQV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 LEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSGL-PELKYLQI 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           316 IFLHSNSIARVGVNDFCPTVPKMKKSLYS-------AISLFNNPVKYWE 357
                                                                                                                                                                                                                                                                                                                                                                                               81; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   74 CPFGCQCYSRV--VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 CPSECTC-SRASQVECTGARIVAVPTPLPWAMSLQILNTHITELNESPFLNISALIALR 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96394313; PubMed=8798419;
Suzuki Y., Sato N., Tohyama M., Wanaka A., Takagi T.;
"cDNA cloning of a novel membrane glycoprotein that is expressed specifically in glial cells in the mouse brain LIG-1: A protein with Jeucine-rich repeats and immunoglobulin-like domains.";
J. Biol. Chem. 271:22522-22527(1996).
                                                                      Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimus
                                                                                                                                                                                                                                                                                                                                                      14.9%; Score 297.5; DB 4; Length 581; 26.4%; Pred. No. 3.2e-13; Live 64; Mismatches 134; Indels 81.
                                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun. 290:756-762(2002).
EMBL; AB071037; BAB84587.1; -.
SEQUENCE 581 AA; 64396 MW; 1F381485BD2CCB54 CRC64;
01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                         MEDLINE=21645900; PubMed=11785964;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380 LPGNIFANVNGLMAIQLON 398
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                                                                                                                                                                                                                                                                                                                                                                                              Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                          TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                Best Local
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                                                        HLIB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 QLDLNRNRIRLIEGLIFQGLDSLEVLRLQRNNISRLIDGAFWGLSKMHVLHLEYNSLVEV 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 KGMNALHVLEMSANPLDNNGI---EPGAFEGV--TVFHIRIAEAKLTSVP-KGLP-PTLL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 ELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKI 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304 PSG-LPELKYLQIIFLHSNSIARVGVN--DFCPTVPKMKKSLYSAISLFNNPVKYWEMQP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277 NSGSLYGLTALHQLHLSNNSISRIQRDGWSFC-----QKLHELILSFNNLTRLDEESL 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 CAAACTCAGNSLDCSGRGLATLPRDLPSWTRSLNLSYNRLSEIDSAAFEDLTNLQEVYLN 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEI----PLNLPKSLAELRIHENKVKKIQKDTF 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 SNELTAI-PSLGTASIGVVSLFLQHNKILSVDGSQLKSYLSLEVLDLSSNNITEIRSSCF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gabs
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Membrane alycoprotein LIG-1.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                             30;
                                                                                                                                                                                                                                                                                                                                                                                                      14.9%; Score 296; DB 11; Length 10 30.1%; Pred. No. 8.8e-13; ive 64; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nilson J., Vallbo C., Henriksson R., Hedman H.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF381545; AAK62357.1; -. InterPro; IPR001606; IQ_MHC. InterPro; IPR001611; IRR. InterPro; IPR001641; IRR. InterPro; IPR0000483; IRR_Cterm. InterPro; IPR000372; IRR_Nterm.
                                                                                                                                                                                                                                                                                                                                                                    1091 AA; 119283 MW; A13D0866CE4C203D CRC64;
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                                                                                  InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR_Cterm.
InterPro; IPR000372; LRR_Uterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
                              MGD; MGI:107935; Img.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
EMBL; D78572; BAA11416.1; -.
                                                                                                                                                                                                                                                                                                                                 LRR_TYP; 4.
                                                                                                                                                                             Pfam; PF00047; 19; 3.
Pfam; PF00560; LRR; 14.
Pfam; PF01463; LRRCT; 1.
SMART; SM0408; IGC2; 3.
SMART; SM00370; LRR; 6.
SMART; SM00802; LRR; 6.
SMART; SM00082; LRR; 7.
SMART; SM00082; LRR; 6.
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Best Local Similarity 30.15
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 AE----LSSLSI 337
                     P56276; 1TLK.
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                                                                                                                                                                                                                                                                                                                                   SMART; SM00369;
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                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 -LPELKYLQIIFLHSNSIARVGVN--DFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATF 363
                                                                                                                                                                                                                                                                                                                                                                                            74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEI---PLNLPKSLAELRIHENKVKKIQKDTF 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 SLYGLTALHQLHLSNNSIARIHRKGWSFC-----QKLHELVLSFNNLTRLDEESLAE- 329
                                                                                                                                                                                                                                                                                                                        24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                14.5%; Score 289; DB 4; Length 1093; 28.5%; Pred. No. 2.8e-12;
                                                                                                                                                                                                                                                                                                                 63; Mismatches 134; Indels
Pfam; PF00047; ig; 3.
Pfam; PF01560; LRR; 14.
Pfam; PF01463; LRRCT; 1.
Pfam; PF01462; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
SEQUENCE 1093 AA; 119052 NW; 8488FA41BB10F353 CRC64;
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Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB050468; BAB40659.1; -.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Membrane 91ycoprotein LIG-1.
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InterPro; IPR003599; Ig.
InterPro; IPR003509; Ig_C2.
InterPro; IPR003800; Ig_L1ke.
InterPro; IPR003000; Ig_MHC.
InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR_Cterm.
InterPro; IPR00372; LRR_Nterm.
InterPro; IPR003591; LRR_typ.
InterPro; IPR03591; LRR_typ.
INTERPRO; IRR_typ.
INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTERPRO*INTE
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SMART; SM00409; IG; 3.
SMART; SM00408; IGC2; 3.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                        88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                    Sest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            364 RCVLSRMSV 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             330 ---LSSLSV 335
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                                                                                                                                                                                                                                                Query Match
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          Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 LDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPSG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 HIRIAEAKLISVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENG 282
                                                                                                                                                                                                                                                         74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
                                                                                                                                                                                                                                                                                 134 NNKLTKIHPKAFLTTKKLRRLYLSHNQLSEI----PLNLPKSLAELRIHENKVKKIQKDTF 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307 - LPELKYLQIIFLHSNSIARVGVN--DFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATF 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 SLYGLTALHQLHLSNNSIARIHRKGWSFC-----QKLHELVLSFNNLTRLDEESLAE- 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                           Gaps
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Moats-Staats B.M., Stiles A.D., Xu L.;
"Expression of decorin RNA in rat lung undergoing chronic lung
                                                                                                                                                           14.5%; Score 289; DB 4; Length 1094; 28.5%; Pred. No. 2.8e-12; Live 63; Mismatches 134; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: L75825; AAA85371.1; -.
InterPro; IPR001561; LRR.
InterPro; IPR001592; LRR_out.
Fram; PF00560; LRR; 2.
SWART; SM00370; LRR; 2.
NON_TER 1 1 1
NON_TER 96 96
SEQUENCE 96 AA; 10398 MW; C6D19F1750B050D0 CRC64;
                                                                                                              1094 AA; 119165 MW; 6B2D0CC3C2783F18 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.4%; Score 287; DB 11; 54.2%; Pred. No. 2.1e-13; iive 20; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283 SLANIPRVREIHLENNKLKKIPSGLPELKYLQIIFL 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
SMART; SM00370; LRR; 5.
SWART; SM00082; LRRCT; 1.
SWART; SM00013; LRRUT; 1.
Immunoglobulin domain.
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Best Local Similarity 54.29
                                                                                                                                                                                                           88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                      Best Local Similarity
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                                                                                                                     SEQUENCE
                                                                                                                                                              Query Match
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                                                                                                                                                                                                           Matches
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Query Match
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Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Ra Aito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Ra Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Ra Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Browstein M.J., Boilunga N., Carninci P., de Bonaldo M.F.,
Ra Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Romstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Autons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Ra Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Ra Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
Mynshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 CPFGCQCYSRV--VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 LNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNL---PKSLAELRIHENKVKKIQKD 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 TFKGMNALHVLEMSANPLD--------ROWNALHVLEMSANPLD-R 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 QFSQFSNLKELQLYGNNLEYIPEGVFDHLVGLTKLNLGNNGFTHLSPRVFQHLGNLQVLR 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 CPSECTC-SRASQVECTGAQIVAMPSPLPWNAMSLQILNTHITTELPEDKFLNISALIALK 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashizaki Y.;
"Functional amotation of a full-length mouse cDNA collection.";
Nature 409:665-690(2001).
EMBL: AK017350; BAB30702.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
5430427N11Rik.
Mus musculus (Mouse).
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=HEAD;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:1921738; 5430427N11Rik.
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InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
Pfam; PP00560; LRR; 11.
PRINTS; PR00019; LEURICHRPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                 Q9D3K0;
                                                                                                                                                                                                  Q9D3K0
                                                                                                                                   RESULT 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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"Distinct but overlapping expression patterns of two vertebrate slit homologs implies functional roles in CNS development and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Holmes G.P., Negus K., Burridge L., Raman S., Algar E., Yamada T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                 264 IFMQLPHLNKLTLFGNSLKELSPGVFGPMPNLREL---WLYNNHITSLPDNAF 313
283 SLANIPRVREIHLENNKLKKIPSG----LPELKYLQIIFLHSNSIARVGVNDF 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112974 MW; 46CD0D5B7246FC72 CRC64;
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PROSITE; PS01186; EGF_2; 7.
PROSITE; PS01187; EGF_CA; 2.
Calclum-binding; EGF_like domain; Glycoprotein; Repeat.
                                                                                                                                                                                                                                                                                  01-WAY-1999 (TrEMBLrel. 10, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Neurogenic extracellular slit protein (Fragment).
                                                                                                                                                                                                      PRT; 1025 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_2.
PROSITE; PS01185; CTCK_1; UNKNOWN_1.
PROSITE; PS01225; CTCK_2; 1.
                                                                                                                                                                                                                                                          01-MAY-1999 (TrEMBLrel. 10, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000152; Asx.hydroxyl.
InterPro; IPR000152; Asx.hydroxyl.
InterPro; IPR000152; Egr-like.
InterPro; IPR001681; Egr-2.
InterPro; IPR001881; Egr-Ca.
InterPro; IPR001481; Egr-Ca.
InterPro; IPR001481; Egr-II.
InterPro; IPR001545; Foln.
InterPro; IPR001791; Laminin_G.
InterPro; IPR001791; Laminin_G.
InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Out.
InterPro; IPR0003591; LRR_Out.
InterPro; IPR003591; LRR_Out.
InterPro; IPR00181; Egr; 9.
Pfam; PF00008; Egr; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99279238; PubMed=10349621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mech. Dev. 79:57-72(1998).
EMBL; AF074960; AAD04345.1; -.
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SMART; SM00179; BGF_CA; 2.
SMART; SM00001; BGF_Like; 7.
SMART; SM00274; FOLN; 2.
SMART; SM00282; LamG; 1.
SMART; SM0370; LRR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00010; EGFBLOOD.
PRINTS; PR00011; EGFLAMININ.
PRINTS; PR00019; LEURICHRPT.
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SWART; SW00082; LRRCT; 2.
SWART; SW00013; LRRNT; 2.
SWART; SW00369; LRR_TYP; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00560; LRR; 7.
Pfam; PF01463; LRRCT; 2.
Pfam; PF01462; LRRNT; 2.
                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:1315205; Slit2.
                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1025 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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SEQUENCE
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DB 11; Length 1025;

14.2%; Score 282.5;

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SEQUENCE
                                                                                Query Match
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                      109 QNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNL 168
                                                                                                                                                                                                                                                                                                                                                                       169 PKSLAELR---IHENKVKKIQKDTFKGMNALHVLEMSANPLDNN-------- 209
                                                                                                                                                                                                                                                                                                                                                                                                                 | :| :::|:: : | :::|: | 1.52 FIGLGSVRLLSLYDNQTTTVAPGAFDXLHSLSTLNLLANPFNCNCHLAWLGEWLRRKRIV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----FHIRIAEAKL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 TSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIHLENNKLKKI-PSGLPELKYLQIIFLHSNSIARV---GVNDFCPTVPKMKKSLYSAIS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.8%; Pred. No. 7.5e-12; vative 65; Mismatches 128; Indels 109; Gaps
                                                                                                                                                                       2 CPEKCRCEGTTVDCSNQRLNKIPDHIPQYTAELRLNNNEFTVLEATGIFKKLPQLRXINF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Foresign of slitter and slit-3 during chick development.";
Lober, Dyn. 222:301-307(2001).
Rober, Dyn. 222:301-307(2001).
Rober, Dyn. 222:301-307(2001).
Rober, Broons and Additional and A
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Pfam: PF01463; LRRCT; 3.
PROSITE; PS00100; ASX_HYDROXYL; UNKNOWN_2.
PROSITE; PS01185; CTCK_1; UNKNOWN_1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS01225; CFCK_2; 1.
PROSITE; PS01186; EGF_1; UNKNOWN_9.
PROSITE; PS01186; EGF_2; UNKNOWN_7.
NON_TER
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                                                                                                     74 CPFGCQCYSRVVHCSDLGLTSVPTNIPFDT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  348 LFNNP------VKYWEMQPATFRC 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----GIEPGAFEGVTV---
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Pfam; PF00054; laminin_G; 1.
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                                      89; Conservative
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      Best Local Similarity
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                                      Matches
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STRAIN-WISTAR RAIS: TISSUE-BRAIN;
MEDLINE-2164900; PubMed-11785964;
SAIOH K., Hata M., Yokora H.;
"A Novel Member of the Leucine-Rich Repeat Superfamily Induced in Rat
                                                                                                                                                                                  168 LPKSLAELR---IHENKVKKIQKDTFKGMNALHVLEMSANPLDNN------- 209
                                                                                                                                                                                                                                                                                                                                                                                        255 VSGNPRCLKPFFLKDIPIQDVDAQDFTCEGNDESSCLLSPPCPSQCTCVDSVVRCSNKGL 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                        Gaps
                                                                                                                                                                                                                                                        108 LQNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLN 167
                                                                                                                                                                                                                                                                                        ----IRIAEAKL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232 TSVPKGLPPTLLELHLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 EIHLENNKLKKIP-SGLPELKYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFN 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : | |:|: | | ::| | 374 TLILSYNRLRCIPVHAFNGLRSLRVLTLHGNDISSVPEGSFNDLVS-----LSHLALGT 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 CPFGCQCYSRV--VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLI 131
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                                                14.2%; Score 282; DB 13; Length 1095; 22.9%; Pred. No. 8.8e-12; tive 65; Mismatches 132; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
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1095 AA; 120689 MW; F6C8B2E483D3A66E CRC64;
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Biochem. Biophys. Res. Commun. 290:756-762(2002).
EMBL; AB071036; BAB84586.1; -
SEQUENCE 578 AA; 64127 MW; 991BD057F5912591 CRC64;
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Last annotation update)
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                                                                                                                                                     73 MCPFGCQCYSRVVHCSDLGLTSVPTNIPFDT----
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                                                                                                     Conservative
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                                                                          Similarity
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                                                     Query Best Local Similar
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                                                                                                                                                261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 CPFGCQCYSRVVH-CSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLIL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 NNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIP---LNLPKSLAELRIHENKVKKIQKDT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 HNNSITHLSADVFSTLPSLRVLDLSSNSLLSLPNEVFSKLKNLKTLIISSNDV-QLGPEC 136
144 QFSQFSNLRELQLHGNNLESIPEEAFDHLVGLTKLNLGRNSFTH--LSPRLFQHLGNLQV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 COSGCKCPTKTTAVCKGSSLRSIPILLDPRTTVLDLSNNRISRLSADELSLYPNLEQLIL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                            202 LRLHENRLSDIPMGTFDALGNLQELALQENQIGTLSPGLFHNNRNLQRLYLSNNHISQLP
                                                                                                                                                                                                                                                               262 PGIFMQLPQLNKLTLFGNSLRELSPGVFGPMPNLREL---WLYNNHITSLADNTF 313
                                                                                                                                                                                                                         281 NGSLANIPRVREIHLENNKLKKIPSG----LPELKYLQIIFLHSNSIARVGVNDF 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C. elegans: a platform for investigating biology, The C. elegans Sequencing Consortium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000483; LRR. Cterm.
InterPro; IPR000483; LRR. Cterm.
InterPro; IPR000372; LRR. Nterm.
InterPro; IPR003592; LRR. out.
InterPro; IPR003591; LRR. typ.
Pfam; PF00560; LRR; 13.
Pfam; PF00463; LRRC; 1.
PRINTS; PR00019; LEURICHRPT.
SMART; SM00370; LRR; 5.
SMART; SM00019; LRRCT; 1.
SMART; SM00013; LRRCT; 1.
SMART; SM00013; LRRCT; 1.
SMART; SM00013; LRRCT; 1.
SMART; SM00014; LRRCT; 1.
SMART; SM00015; LRRCT; 1.
SMART; SM00015; LRRCT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kohara Y., Shin'i T., Suzuki Y., Sugano S., Potdevin M., Thierry-Wieg Y., Thierry-Mieg D., Thierry-Mieg J.; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. EMBL; ACO242013 ARF3602011; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston R.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.1%; Score 281; DB 5; 26.5%; Pred. No. 4.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              investigating biology. The C.
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y71F9B.8 protein (1D304).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y71F9B.8 OR 1D304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9N4G6;
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                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 47
                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9N4G6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HID DESCRIPTION OF STREET 
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RAX Adams W.D. Celniker S.E. Holt R.A., Evans C.A., Gocayne J.D., RA Adams W.D. Celniker S.E., Holt R.A., Fry, Hoskins R.A., Galle R.E., Adams W.D. Celniker S.E. Li P.W. Hoskins R.A., Galle R.E., George R.A., Lewis S.E., Li P.W., Hoskins R.A., Galle R.E., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Baradon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pefelffer B.D., Ray Baradon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pefelffer B.D., Bardon R.C., Boudwin D., Bolshakov S., Balter H.J., Andrews-Pichankov S., Balthakov S., Borthar J., Borthar J., Brotchan M.R., Bouk J., Brokstein P., Brottler R., Charry J.M., Cawley S., Dalkov B.C., Dunn P., Bortkova D., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Acherry J.M., Cawley S., Dalkov B.C., Dunn P., Botherry M., Cawley S., Dalkov B.C., Dunn P., Botherry M., Cawley S., Dalkov B.C., Dunn P., Botherry M., Cayley S., Carral J.H., Gadlou R., Harris M., Leinar M.E., Gorge I.H., Garg N.S., Gelbart W.M., Glasser K., RA Goog F., Gorrell J.H., Gu. Gann P., Harris M., Harvey D., Helman T.J., Hernandez J.R., Houck J., Harris M., Harris M., Harris M., Harris M., Harris M., Mayley B., Millina N.V., Match B. McIncosh T.C., Morted M.P., Index M. Match B. McIncosh T.C., Morted M.P., Pull Y., Reasel M.G., Reinert K., Remington K.A., Mixon K., Nusskern D.R., Poll Lar, S., Shell T., Ranger B., Spier B., Speidling A. Weinschel M., Stupsk M. Murphy B., Murphy D., Wang S., Yao, R. A., Shin T., Ranger B., Spier E., Spradling A. Weinschel M., Stupsk M., Williams S.M., Woodage T., Weinschel M., Stupsk M., Williams S.M., Woodage T., Worley K.G., Wu B., Zhun S., Zhon R., Shier R., Zhong W., Zhun S., Zhan R., Zhong W., Zhun S., Zhan R., Zheng S., Zhong S., Zh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).

Bukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                               255 NTWSLPALKTLDLSSNLFVSLETASFDGLPALQYLNISHSRNLKTIQMATFVQLSSLHWL 314
246 HLDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIP- 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                  ----SGLPELKYLQI-----
                                                                                                                                                                                                                                                                                                                                    317 FLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKY 355
                                                                                                                                                                                                                                                                                                                                                                                                             315 SISSSALTHIHPSAFNPIPP-----LSHLDLSNNELRY 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1513 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=BERKELEY;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CG5195 protein.
CG5195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OBVPFO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 48
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"Cloning and characterization of the rat gene for the acid-labile
ry subunit of the insulin-like growth factor binding protein complex.";
J. Mol. Endocrinol. 19:267-277(1997).

BMBL; AF006203; AAC15252.1;

RIGETPO: IPR001611; LRR.

InterPro: IPR000483; LRR_Cterm.

R InterPro: IPR000372; LRR_Cterm.

R InterPro: IPR003591; LRR_Ltp.

R InterPro: IPR003591; LRR_Ltp.

R Fram: PF00560; LRR. 19.

R Pfam: PF001463; LRR.T; 1.

R Pfam: PF01462; LRRNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        600 ELRNLNLQSNKLEAITDNFFSNNSRLEQLDLSRNLIRSISPTAFDTQRSLEYLDLSGNAL 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 ISTVELEDFKRYKELQRLGLGNNKITDIENGSLANIPRVREIHLENNKLKKIPS-GLPEL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 KYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRM 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 DTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----KSLAELRIHENKVKKIQKDTFKGMNA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LHVLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGL---PPTLLELHLDYNK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.9%; Score 276.5; DB 5; Length 1513;
26.8%; Pred. No. 3.2e-11;
Live 66; Mismatches 114; Indels 41; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Insulin-like growth factor binding protein complex acid-labile
                   InterPro; IFROOD191; LIR.Cterm.
R InterPro; IFROOD192; LRR_cterm.
R InterPro; IFROOD192; LRR_cterm.
R Pfan; PFOOT660; LRR; 25.
R Pfan; PFOOT603; LRRCT; 1.
R PRINTS; PROOD19; LEURICHRET.
R SMART; SMO0370; LRR; 5.
R SMART; SMO0369; LRR, 5.
R SMART; SMO0369; LRR, 7.
R SMART; SMO0369; LRR, 7.
R PROSITE; PSOOL16; DNA_POOLYMERASE_B; UNKNOWN_1.
R PROSITE; PSOOL16; DNA_POOLYMERASE_B; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                603 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98121980; PubMed=9460648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81; Conservative
InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 SEIPLNLP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ::
AI 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          371 SV 372
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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070211
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DDC (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ32082 fis, clone OCBBF2000231, weakly similar to phospholipase
A2 inhibitor subunit B precursor.
                                                                                                                                                                                                                                                                                                                                                                       102 DTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQL 161
                                                                                                                                                                                                                                                                                                                                                                                                                     Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokol T., Kodaira H., Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamanoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamanoto J., Warashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Kanehori K., Takahashi-Fuli A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 SEI------PLNL-----PKS-----LAELRIHENKVKKIQKDTFKGMN 194
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                          64;
                                                                                                                                                                                                                                     Length 603;
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"NEDO human cDNA sequencing project.";

bubmitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AKO56644; BAB71240.1; -.

R InterPro; IPR0001511; LRR.

R InterPro; IPR000151; LRR.

R InterPro; IPR000151; LRR.

R Ffam; PF00560; LRR; 9.

R Pfam; PF01462; LRRNT; 1.

SOM SEQUENCE 522 AA; 58628 MW; 73000472E124245C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.8%; Score 275; DB 4; Length 522; 26.8%; Pred. No. 1.1e-11; Indels tive 54; Mismatches 115; Indels
                                                                                                                                                                                                                              13.9%; Score 276; DB 11; Length 60 28.2%; Pred. No. 1.2e-11; tive 58; Mismatches 107; Indels
SMART; SM00370; LRR; 5.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRLT; 1.
SMART; SM0001369; LRR_TYP; 9.
SEQUENCE 603 AA; 66924 MW; 9E8DEC7A9A2315FF CRC64;
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Matches 84; Conservative
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                                                                                                                                                                                                                                                                    Best Local Similarity
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	Search completed: January 24, 2003, 12:26:42	rch cc	Sea
	275 VFETVPHLQSLQL 287	275	QQ
	362 TFRCVLSRMSVQL 374	362	δλ
74	IQ	225	QQ
51	4 P-SGLPELKYLQIIFLHSNSIARVGVN-DFCPTVPKMKKSLYSAISLFNNPVKYWEMQPA 361	304	δy
224		166	Dp
)3	4 ELHLDYNKISTVELEDFKRYKELQRLGIGNNKITDIENGSLANIPRVREIHLENNKLKKI 303	244	Qy
165	130NTTFRPMPNLRSVDLSYNKLQALAPDLFHGLRKLTT 1	130	qq
243	VFHIRIAEAKLTSVPKGLPPTLL	184	Qy
129	88 LMQLTWLYLDHNHICSVQGDAFQKLRRVKELTLSSNQITQLP1.	88	qq
33	124 LTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVK 183	124	Ωy
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